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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
             Score
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1 cgcggctgtcggag
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(without alignments)
11877.277 Million cell updates/sec
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             Description
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SOURCE
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Ebkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ebrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 3896)
1 (bases 1 to 3896)
                                                                                                                                                                                                                                    AF326768 3896 bp mRNA linear Oryza sativa embryonic flower l-like protein mRNA, AF326768 1 GI:15430698
2 (bases 1 to 3896)
Moon, Y.-H., Chen, L.
Direct Submission
                                                               Emf1, a novel protein involved in the and flowering in arabidopsis plant Cell 13 (8), 1865-1875 (2001)
                                                                                                                                                                                                          Oryza sativa.
                                                                                                         Aubert,D., Chen,L., Moon,Y.H., Martin,D., and Sung,Z.R.
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SH1UL45A
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AB010068
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AC079533
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AR203526
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AL591122
AL591122
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AP005444
AX083744
AX083744
AC087825
             Sung, Z.R.
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PLN 05-SEP-2001 complete cds.

AF326768 Oryza sat AP32678 Oryza sat AP001859 Oryza sat 16494 Sequence 14 AC026135 Homo sap1 AC029295 Homo sap1 AC029295 Homo sap1 AC025845 Homo sap1 AC025845 Homo sap1 AC025845 Homo sap1 AC02786 Pseudorabbe AC10786 Pseudorabbe AC10786 Mus muscu AL133232 Human DNA AC007926 Trypanoso AC097681 Rattus no AC103138 Pattus no AC103136 Drosophil AC02786 Drosophil AC02786 Botrytis AC0161518 Homo sap1 AL111116 Botrytis AC016518 Homo sap1 AC111116 Botrytis AC016518 Homo sap1 AC10476 Homo sap1 AC10476 Homo sap1 AC104376 Homo sap1 AC104376 Homo sap1 AC104376 Homo sap1 AC104376 Homo sap1 AC023803 Mus muscu m AC023803 Mus muscu m AC023803 Homo sap1 AC023803 Homo sap1 AC023803 Homo sap1 AC023803 Homo sap1 AC03513 Homo sap1 AC023514 Homo sap1 AC023514 Homo sap1 AC03515 Homo sap1 AC03515 Homo sap1 AC03515 Rattus no AL596170 Listeria AV23518 Caenorhabdi AC015272 Homo sap1 AC03555 Rattus no AB010658 Araboldops AL034559 Plasmodiu AP269518 Staphyloc

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FEATURES
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Best Local Sim
Matches 3894;
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                                                              attttccatgaccagaaaaatgtgatgaacacaaagctagttcaagcccattttctgta
                             ATGGAGATTGTTGCAGTAGATCAGGAGGGAGCTCGTGTTGTTGGGACGAACTGTATGCTT
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ilarity 99.9%;
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TQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAARANTDSPMKDLQGPAQNYDVAA
NVSEDNTSVDVGALPEVPQITWHIEVNGADOPPSTRLSETVULKREDENGKTEETLV
AEQCHLTKDPAPPMSGKRETAQADVSDAKLCRRKPKVVLLSETVNANQYEDSRSDEVH
KRKTDKKLMKKQQHSKKRTAQADVSDAKLCRRKPKVVLLSETVNANQYEDSRSDEVH
RENAADPCEDDRSTIFVPMEVSMDIFVSNHTVGEDGLKSSKNETKRYSDVVDGSSL
KRKTDKKKRGGAVHFTVAHPAANLSNKKVTPFASTQHDDENDTENGLDTNMHKTDVC
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OHVSEISTQRCSSKGKTAGLSKKKTHSAASTKYGGESTRNGQNIHVLSAEDQCCMETE
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NSVLSHSAKVSPAEHDIQSTTISSDCVITVAAKDGSDYASSVEDTNSQQKSLAS
STQKELQGHLALTTQESPHPONFQSTQEQOTHLRMEEMVTIAASSPLESHHDDQYIA
EAPTEHWGRKDAKKLTURDFSTLATMESAKCLOBRNAGGVVLYEKESMFATH
LLRMMDPSTLASFPNYGTSSRNQMESQLHNSPANGYSTSYGSNLNGKIPLTF
EDLSRHQLHDLHRPLRPHFRYGVLGSLLGKEIANWSENCETQSGYKLGVSTGTTSHQM
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RQDICITNKNPADFTTISNDNEYMDYR"
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/db_xref="taxon:4530"
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2700		2641	
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2640		258:	
2580	aaggccactacaagaaattctccagcagcaacatgtggtgctcaatttagacctggtatc	2521	pb
2580		2521	Qy
2520	gaagcaccaactgaacattggggccgtaaggacgcaaagaagctaacgtgggagcaattt	2461	ρ Q
2520		2461	
2460 2460	atggtcactattgctgcaagctcaccactattttcacatcatgatgatcagtatattgct 	2401	p Q
2400	ccacatcctcagaactttcagtctactcaggaacagcagacacatttgcggatggaagaa	2341	d
		2341	Q
2340	gcatcccaaagtacacagaaggagttacagggtcatttggcattgaccacacaagagtct	2281	D Qy
2340		2281	
2280 2280	aaggatggttcagattatgcatcaagtgtgtttgacactaattcccaacagaagtccttg 	2221	p Q
2220	gacatcaaccgtattcaatccaagacaactgctgatgatgatgatgttatagtagttgcc	2161	gb
2220		2161	Qy
2160	. gttgaactgotagotaaaaaccagoatgagaggcagottatgactgagactgattgttct	2101	D 04
2160		2101	
2100 2100	. caaaaacttgaagtgactogtgaaaaacagaccatgatagatgacatccccatggatatt 	2041	Ωу
2040	. catgatatccaaattatgtctgaccttcatgagcagagtctacccaagaagaaaaaagaag	1981 1981	рь
1980	. tgccagatggaaaccgaaaactctgttctgagtcactcggcaaaggtttctcccagctgag	1921	p 0y
1980		1921	
1920 1920	. tatggtggtgaaagcaccagaaatggtcagaacatacatgtactcagcgcagaagatcaa 	1861	B &
1860 1860	. tcaaaggggaaaacagcgggtttgagtaaggggaaaacacattcagctgctagtaccaaa 	1801	B 8
1800 1800	atatgcataagacagatgtctgtcagcatgtatcagaaatctccacacagaggtgctca	1741 1741	Db Qy
1740 1740	acacccactgcgagtactcagcatgatgatgagaatgatactcaaaatggtcttgacaca	1681	р _р
1680	actggaagtgtgcatcacacagttgctcatccagctgggaatttgagcaacaaaaagtg	1621	ОУ
1680		1621	

3840	$cgagaaatggttttgtcggtgttaaggttgaaacgactagctctcgttatcaatgtgttg \\ .$	3781	Qy
3780	AGTGTTGTGAGCTGTGTGACTGACGG	3721	DЬ
3780	cccattttgtaattaccataaggaggtttatagtgttgtgagctgtgtgtg	7	Ωу
3720	ACTAGTGCGCTTGTTTGTACAAGGAGAAATGTGTAACCTTGTTGAAAAAAATGTC	3661	дь
3720	atactagtgcgcttgtttgtacaaggagaaatgtgtgaaccttgttgaaaaaatgtctc		Оу
3660	CATCCGGTTTTTGTTTTGCCAGTCCAAGAAACGTCCTCCTGTTACTTTGTAGTTGTACT	3601	ДЪ
3660	gcatccggtttttgttttgccagtccaagaaacgtcctcctgttactttgtagttgtact	3601	Qy
3600	ATGCCCCATTTTCTGGATGGGAACCTGCCAGACAGTGAACAAGGGCTTTGCAAGGTGC	3541	Ф
3600	gatgccccattttctggatgggaacctgccagacagtgaacaagggct1:tgccaaggtgca	3541	Оу
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3480	AGTGGTGTGCATAATTCCTGAACATTTACAATCATACATTTCATCTTTATGGCGCCCAAA	4	Db
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3420	CCAGCTGATTTTACTACAATCAGTAACGATAACGAGTATATGGATTACCGCTGAAGCAGA	3361	Дb
	cagctgattttactacaatcagtaacgataacgagtatatggattaccgctgaagcaga	3361	Qy
3360	AAAATGGTTCATCCCTTGGATCGGTTTGTGAGACAGGATATCTGTATAACTAAC		Дb
3360	ntggttcatcccttggatcggtttgtgagacaggatatctgtataactaac	3301	Qy
3300	AGTGCATATTTTTTATCAGCGAGGAACAGCATAGCTCAATCTTGGACCAGAGGCAAGGGT	3241	рь
3300	gtycagattttttatcagcgaggaacagcatagctcaatcttggaccagaggcaagggt	24	Qy
3240	CTGAATTCTGGAATGTTTTCAGCAAAATGGAATGCATTGGGTTGGGTTCTGTTAGCTCC	3181	Db
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3180	TTAGGAGTGTCAACAGGAATAACATCGCATCAGATGAACAGAAAGGAACATTTTGAAGCC	3121	DЬ
3180	taggagtgtcaacaggaataacatcgcatcagatgaacagaaaggaacattttgaagcc	3121	Оy
3120	TTGCTGCAGAAGGAAATTGCAAACTGGTCGGAGAACTGTGGCACACAATCTGGTTATAAG	3061	ф
3120	gctgcagaaggaaattgcaaactggtcggagaactgtggcacacaatctggttataag	3061	Qy
3060	CAGCTGCATGATCTGCACAGACCTTTACGCCCCACATCCTAGAGTTGGTGTGCTTGGCTCC		ФФ
3060	ctgcatgatctgcacagacctttacgcccacatcctagagttggtgtgcttggctcc	3001	Qy
3000	TCATATGGCAGTAACCTGAATGGAAAGATTCCATTGACATTCGAAGACTTATCACGGCAT		Ф
3000	catatggcagtaacctgaatggaaagattccattgacattcgaagacttatcacggcat	2941	Qy
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2760	gaaattttccaagcacaatagcaaccatggaagcgagtaagttatgtgatcggagaaat	2701	Оу

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RESULT
AP001859
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3841 taaacttctagattgatgtgttaccttactcttgaagtcaacaccggagaatttac 3896
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AP001859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The orientation of the sequence is from T7 to SP6 of the PAC clone. The orientation of the sequence is from T7 to SP6 of the Genes were predicted from the integrated results of the Gelnes were predicted from the integrated results of the SP1 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MARF DNA bank and the cDNA sequence database at RGP. Protein similarities of the coding regions were searched against NRP with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Varnolionhyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and RGP clone ID.

This sequence of this clone has an overlap with P0431F01 clone, This sequence of the 3' end. This clone ends at the position 57,376 DDBJ:AP001550 at the 3' end. This clone ends at the position 57,376 of P0431F01. Detailed information on overlap and assembly quality together with annotation of this entry at together with annotation of this entry at the sequence with annotation of this entry at together with annotation of the sequence of this clone ends at the position of the sequence of the sequence of this clone ends at the position of the sequence of this clone ends at the position of the sequence ends at the position of the sequence of this clone ends at the position 57,376 of position of position of the sequence ends at the position 57,376 of position of position of position of the sequence ends at the position 57,376 of position 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-APR-2000) Takuji Sasaki, National Institute
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         .10850,10933.
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TRRSTKGNWTPEEDAILSRAVQTYNGKNWKKIABCFPDRTDVQCLHRWQKVLNPELVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPWSKEEDEIIVQMVNKLGPKKWSTIAQALPGRIGKQCRERWYNHLNPGINKEAWTQE
EEITLIHAHRMYGNKWAELTKFLPGRTDNSIKNHWNSSYKKKVNSYMSGCLLTQYSCL
PLNEYSANCNSSPAMTQQNSEDSGCFAVREVENSSGCSQSSLAKVSCSQVHDTTVPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="51milar to Arabidopsis thaliana chromosome/note="51milar to Arabidopsis thaliana chromosome/note="51milar to myb-protein" (AL022537)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEARS AT PAPENS DE L'AUTE L'ALTELLETA I KNCGDIFHMHVAERDVLHERVK LYKKKSDONVKEKV KRIGHKNPKVQILALTLLETA I KNCGDIFHMHVAERDVLHERVK LYKKKSDONVKEKV KRIGHKNPKVQILALTLLETA I KNCGDIFHMHVAERDVLHERVK LYKKKSDONVKEKV KRIGHKNPKOGPARAT POYYTAAYHDLVRACAAF PKRSDRPAP LENGQSPAGRNMRS PDQDEARSSAS AGNDFPALSMSEIQNARGIMVLAEMLNALDPGNREGLRQEVI VELVO QCRIYKQRVVLLVNATADEELMSQGLALNDDLQRVLAKHDALAGALAVRUEKKPKSLQ ALVDIEDSMNQDSKKEQALVDI EDPTTGETNKEPSQSASYQSPFEQLALPAPPVSNGS ALVDIEDSMNQDSKKEQALVDI EDPTTGETNKEPSQSASYQSPFEQLALPAPPVSNGS ALVDIEDSMNQDSKKEQALVDI ESQNNTI NILAKPADAPEGVNSSSTLPGSQPYNAPTQHPLQAQQQPQVGLYPNGGAVNPGTSYPT NNILAKPADAPEGVNSSSTLPGSQPYNAPTQHPLQAQQQPQVGLYPNGGAVNPGTSYPT NNILAKPADAPEGVNSSSTLPGSQPYNAPTQHPLQAQQQPQVGLYPNGGAVNPGTSYPT NNILAKPADAPEGVNSSSTLPGSQPYNAPTQHPLQAQQQPQVGLYPNGGAVNPGTSYPT NNILAKPADAPEGVNSSSTLPGSQPYNAPTQHPLQAQQQPQVGLYPNGGAVNPGTSYPT NNILAKPADAPEQVNSSSTLPGSQPYNAPTQHPLQAQQQPQVGLYPNGGAVNPGTSYPT NNILAKPADAPEQVNSSSTLPGSQPYNAPTQHPLQAQQQPQVGLYPNGGAVNPGTSYPT NNILAKPADAPEQVNSSSTLPGSQPYNAPTQHPLQAQQQPQVGLYPNGGAVNPGTSYPT NNILAKPADAPEQVNSSSTLPGSQPYNAPTQHPLQAQQQPQVGLYPNGGAVNPGTSYPT NNILAKPADAPPQNGAVNPGTSYPT NNILAKPADAPPQNGAPPQNGAPPQNGAPPQNGAPPQNGAPPQNGAPPQNGAPPQNGAPPQNG
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LAHIHIQVGVKTVRKPSLSFSFSYFEFGIEIGNSGYENGIEYYRNRKWSENEPAQIR'
join(23045...23145,24592...24670,25118...25216,25302...2541
25608...25750,26364...26445,27073...27158,27527...27760,
29332...29917)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region of the predicted gene.
Similar to Caenorhabditis elegans chromosome 3, cosmid C17G10; alcohol dehydrogenase/ribitol dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTTEQTKDGQSAGNDEHMDEGTTGERSSATNVATNDDLSGNLVSTSSF"
complement(join(18608..18823,19905..20031,20072..2022
20774..21113,21407..21738,21975..22508))
/note="ESTS AU082761(S5084),D42006(S5084) correspond to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLTQSVTAPDEQDKGALFYEPPREPSLDVPFVSCDLVTSGDLQEFSPLGIRQLMHSTM
NVCTPMRLWGSPTHDESTGVLLKSAAKSFICTPSILKKRHRDLLSPIPDKRIEKKYGT
EKDRGVSDTSSTGIOTSCINATKDDALITTVLRIERSASSKSLEKKLVFSDENKENLG
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AEVVTQSSSSSGDAEMFANPGCSNDRHVPSSTMESIPECGDQQVTNAEEFPEASLEKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDLQVNANFDKNEAHDSQSSMGPQACYTSAEAVASALPAVHCHVSSSNLDPDQHLQED
FAQGLNLDMTIDEMPTVPSFADNQTVCSIENHERSLEPYDVAMEVPLSMLSSDSGAEQ
KLHFMSEADFNSPNCLKSELMQDISLQGLLSGPDAVEADSISRSNHQSDVYSSEADTH
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IHQMYEGGFQRLSDRLFRDAPWPAAEAVSPYCDGDHVFLLLYELWYRHAYARASSS
SSSAPLTAGGRAESWANYCDLFSVVLHGVVNNQLPMQMLWDWDDEFVYQFQSFCQYRA
KLKNKSDDELHQLKQFDKAWNYGVLNYLQALVEKSMIAQIILEREKECLEQFTATDGY
DYQGGSNVLKMLGYYSMIGLLRIHCLLGDYRTGLKCLAPIDLNQQGVYTIVIGSHISA
IYHYGFANLMMRRYAEAIREFNKILLYILKYKQYHQKSPQYDQILKKKEQMYAFLAVC
IYHYGFANLMMRRYAEAIREFNKILLYILKYKQYHGKSPQYDQILKKNEQMYAFLAVC
ISLCPQHNLIDENVSTQLKEKYNDKMYKMQRFDEETYAAYDELFSYACPKFITPSPPA
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                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA94772.1"
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QPSPMPGAQPVMMYAQPMMPSSYMGMNSSPYSTTPSSSSSMGQPSKPEDKLFGDLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein"
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/protein_id="BAA94771.1"
/db_xref="GI:7630238"
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/protein_id="BAA94770.1"
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/note="ESTs AU031545(E61825),AU031546(E61825) correspond
                                                                                                                                                                                                                     complement(join(34629. .34795,36831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="Similar to Arabidopsis thaliana chromosome 2 BAC 19C21; unknown protein. (AC004683)"
/protein_id="BAA94773.1"
                                                                                                             /note="hypothetical protein"
                                                                                                                                                                                                                                                                                              LAKTKQNKA"
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CDS

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Ouery Match 75.8%;
Best Local Similarity 87.4%;
Matches 3487; Conservative
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                                                       386
ATGCATCTTTATAATGATAATCTTATTTTTCTTGTACCAGAGGGTATGTTGCTCCTTCTTC 54103
                            acgaaccggcacaacaccaatgcgagcatttctccataagagggtatgttgctcttcttc 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGCPMEXDLIFWTHERGROVKADEEVRGSRSARTELK IRGVGLML/DGGYPFILVANG
FMCVRAVLHRWGSNGGRLALLTCSLTKANCLLAMKFLFREKOTFELGNIEEAAASG
FMCVRAVLHRWGSNGGRLALLTCSLTKANCLLAMKFLFREKOTFELGNIEEAAASG
ERSTARTVDRAPPERLARGCGSKRKPBGG-ALSGLELLAASMGTKALIFHVAEEKKIPSF
AGILAATFWGNLFLAIILPARISGALIFHELIEVDIYCACLCVDSLLVVVIDMEIVAV
DQEGARVVGTNCMLARGGTGAVAPVLELTATPRODAALEAGVDEPAQHOCEHFSIRGY
VALLQKKDPKRCSLSRIFHDOKKCDEHKASSSPSYAAKFRRWDCSKCLDKLKTSDNGT
APTILFAKQNGTSDGCSITFVRSTFVPASVGSQKVSPSYQSGCKNADRSTLPKSVQE
GNDSKCNAPSGKNGAAEANTDSPMKDLOGPAQNYDVAANVSEDNTSVDVGALPEVPQI
TWHIEVMGADAPPSTKLSEVVLKRNEDENGKTEETLVAECOLLTKDPNMSGKERDO
VAEQCNLTKDPKPVSGOKCEQICNEFCEVVLKRSSKSKRKTDKKLMKKOQHSKKRTA
QADVSDAKLCRRKPKKVRLLSEIINANQVEDSRSDEVHERAAADPCEDDRSTIPVPME
VSMLIFVSVNITYWGBOCLKSSKNKTKRKYSTSDVDDGSSLMNWLNGKKRTGSVHHTVAH
PAGNLSNKKVTPTASTQHDDENDTENGLDTNMIKTDVCHVSEISTQRCSSKKKTAGL
SKKTTBADDCVIVAAKDGSDTASSVFDTNSQOKSLASNGHERQLHTETDCSDINR
IQSKTTADDDCVIVAAKDGSDTASSVFDTNSQOKSLASOSTQKELGGHLALTTQESPH
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PQNFOSTQBEDGTAGRANDTASSPLFSHDDOYLASOSTQKELGALATTGESPH
PQNFOSTQBEDGTAGRANDTASSPLFSHDDOYLASOSTQKEDAKKLTWREOF
FRATTENERGALTGCAGEDGTAANSSPLFSHDDOYLASOSTQKEDAKKTAGLALTTQESPH
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Join(67330..67530,67676..67816,69073..69234)
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/note="Similar to Arabidopsis thaliana
F19F19; unknown protein (AC000104)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(58634. .58667,58796. .58902,59018. 59368. .59432,59585. .59648,60333. .60442,60620. .60835. .60945))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNQMESOLHNSOYAHNOYKGSTSTSYGSNLNGKIPLTFEDLSRHOLHDLHRPLRPHPR
VGVLGSLLOKEIANWSENCGTQSGYKLGVSTGITSHOMNRKEHPEALNSGMFSAKWNA
LOLGSVSSSADFLSARNSIAQSWTRGKGKMVHPLDRFVRQDICITNKNPADFTTISND
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WICAPVVAAAWICAPASPVPDGVSPSCLRAVPPPPNRRQTRPSVVAPSPTIDRHIPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(46367. .46423,47537. .47769,48031. :48153,50082. .5
51762. .51864,52091. .52204,52433. .52532,22784. .53004,
54084. .54514,54601. .55709,56020. .57468)
/note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"ESTs AU082698(R0665), D23963(R0665) correspond to region of the predicted gene. Similar to Arabidopsis thaliana rac GTP binding protein Arac7. (AF079484)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIAPLDRYAERAVNQV
HARNFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYGTSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAA94776.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                 .70236,70344.
                                                                                                                                                               DB
                                                                                                              23;
                                                                                                                                                                  8
                                                                                                                                                               Length 150594;
                                                                                                                                                                                                                                                                                                          chromosome 1
                                                                                                                                                                                                                                                                                                                                 .70514)
                                                                                                           481;
                                                                                                        Gaps
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AAGATCA 556	ATGGTGGTGAAAGCACCAGAAAATGGTCAGAACATACATGTACTCAGCGCAG	55604	В
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REFERENCE
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                                                                                                        Unclassified.
1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                                                                         Biren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Sanderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T., Mihoya, T., Mitanda, C., Mlenga, V., Morrow, J., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Voung, G., Zalnoun, J., Zimmer, A., and Zody, M.
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Submitted (19-MAR-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 5, 2000 this sequence version replaced g1:7264205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 141041)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 3, clone RP11-78022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                    Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
RP11-78022
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map 3,
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FEATURES
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center project name: L7353
Center clone name: 18_0_22
Center clone name: 78_0_22
Sequencing vector: M13; M79815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Censensus quality: 132847 bases at least Q40
Consensus quality: 132847 bases at least Q30
Consensus quality: 139005 bases at least Q20
Insert size: 145000; agarose-fp
Quality coverage: 4.8 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
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109946 141041
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19509 26115: contig of 6607 bp in length
26116 26215: gap of 100 bp
26216 39655: contig of 13440 bp in length
39656 39755: gap of 100 bp
39756 54129: contig of 14374 bp in length
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2191 2290: gap of 100 bp
2291 5642: contig of 3352 bp in length
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14920. .19408
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                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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  /note="assembly_fragment"
19509. .26115
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                                                                                                                                                                                  AUTHORS
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hes 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAACAAAATTGATTCTATTGAAAATTCATA 98674
                                                                                                                                                                                                                                                                                                                                                     ACU92925 141095 bp DNA linear H
Homo sapiens chromosome 3q clone RP11-78022, WORKING
SEQUENCE, 10 unordered pieces.
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Auzny,D.M., Adams,C., Adio-Oduola,B., Are,J.R., Banks,T., Barbaria,J., Alstrooks,S.L., Amaratunge,H.C., Are,J.R., Bonks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Cher, E., Chowdhry,L., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Davy-Carroll,L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo: 1 (bases 1 to 141095)
                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT
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/note="assembly_fragment
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109946. .141041
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Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Gall, R., Garrer, T., Garcia, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Helins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jackson, L., E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Moris, S., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Moris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Ovledo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Stone, H., Tansey, J., Taylor, C., Taylor, T., Taffrod, B., Thomas, N., Wardh, A., Swarek, A., Tabor, P., Tamerisa, K., Thomas, S., Walliams, G., Williamson, A., Washington, C., Wart, R., Wooden, S., Walliams, G., Williamson, A., Washington, O., Nelson, D., Weisson, D., Williamson, A., Washington, C., Warten, R., Washington, S., Walliamson, A., Washington, S., Nelson, D., Weisson, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 141095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 0.990329
Consensus quality: 133822 bases at least Q40
Consensus quality: 137507 bases at least Q30
Consensus quality: 138991 bases at least Q30
Consensus quality: 138991 bases at least Q30
Estimated insert size: 139059; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 4.8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: HCXD Center clone name: RP11-78022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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                                 34365
34465
69011
69111
84564
84664
99241
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69010:
69110:
84563:
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                                                           : contig of 34364 bp in 1
gap of unknown length
b) contig of 34536 bp in 1
gap of unknown length
contig of 15453 bp in 1
gap of unknown length
b) gap of unknown length
contig of 14577 bp in 1
of
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                                                                                                                                     length
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                                                                                                                                                                          COMMENT
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                                                                                                                                                                                                                                                                                                                   TITLE
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JOURNAL REFERENCE AUTHORS

JOURNAL

COMMENT

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REFERENCE
AUTHORS
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SOURCE
ORGANISM
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AL591122/c
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                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11650 CTGATGGAGAAAATCTGTAAAGCTGATTAAATATTCATTTAATAGTTG!TCCTGAAGATA 11591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11770 AAAAAAGTAAATTGGCATTAGGAAAAACATTGTAAAGGAAGAGGGTAAATAGTTAACAA 11711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1478 taagcatggatattcctgttagcaaccatacagtgggagaagatgggttaaaatcaagta 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1418 gtgaaaatgccgctgatccctgtgaggatgatagaagtaccatcccggtcccgatggaag 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 1.28;
Local Similarity 46.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atactgaaaatggtcttgacacaaatatgcata 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACATTGAAGCAACAAAACAGAAAAAATTATTAAAAATTACAATTATCAAAATATTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ggctgaatggaaaaaagaaactggaagtgtgcatcacacagtttgctcatccagctg 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agaacaagacaaaacgcaaatactctgatgttgtagatgatgatgatcatcacttatgaact 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggaatttgagcaacaaaaagtgacacccactgcgagtactcagcatgatgatgagaatg 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAGAAAATCAAAACCAAACCAGTTAGACTTAAAAAAAGATATTAAAAAAGATTTGAAAAC 11651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAAACAAAATTGATTCTATTGAAAATTCATA 11498
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                                                                                                                                                                                                                                                                                                                                                                                                                         AL591122 189409 bp DNA linear HTG 18-JAN Homo sapiens chromosome 1 clone RP11-415K20, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                               Center: Wellcome Trust Sanger Institute
                                                                                                         Submitted (17-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: Canabridgeshire, CB10 15A, OR. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 12, 2001 this sequence version replaced gi:16304972.
Contact: humquery@sanger.ac.uk
                                            Center code:
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              HTG;
                                                                                                                                                                                                                                                                                                                                                                                   AL591122.13 GI:16904444
                       Web site:
                                                                                                                                                                                                     Direct Submission
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123171
123271
123271
129354
129454
134226
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                                                                                         ---- Genome Center
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/db_xref="taxon:9606"
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                     http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109723: gap of unknown length
123170: contig of 13447 bp in 1
123270: gap of unknown length
129353: contig of 6083 bp in lei
129453: gap of unknown length
134225: contig of 4772 bp in lei
134325: gap of unknown length
136399: contig of 4374 bp in lei
136799: gap of unknown length
141095: contig of 2296 bp in lei
                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
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FEATURES
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                                                                                                                                                                                                                                                                                                       Db 137147 ATAGCGATGCAGCGAAGCTGGATGGAGCTGGTGCACCAGGGGTGGACGGAACGGATGCAC 137088
                                                          RESULT 7
AC055845/c
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                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: XGAP4; version 4.5

Sequencing vector: M13; M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Chemistry: Dye-terminator Big Dye; 9% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 187859 bases at least Q40
Consensus quality: 188342 bases at least Q30
Consensus quality: 188372 bases at least Q20
Insert size: 189209; sum-of-contigs
Insert size: 199247; L3% error; agarose-fp
Quality coverage: 10.90x in Q20 bases; sum-of-contigs Quality
coverage: 10.95x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                              gtqqtqgaactqqtqctqtaqcgccaqtqttqqaqctgacaqcgacgcctcqtcaqqatq 364
                                                                                                                                               GAGCTGATGCACCAGGGGTGGACGGAGC 137000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: bA415K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. The true order of the pieces * is not known and their order in this sequence record is
Homo sapiens chromosome 11 clone RP11-682B13 map 11, IN PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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128166 187247: conti
187248 187347: gap of
187348 189409: conti
                                                                                                                                                                                                                                                                                                                                                                                          1.2%;
nilarity 57.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector_side:left"
128166. .187247
128166. .187247
/note="assembly_fragment:04137
fragment_chain:1"
187348. .189409
/note="assembly_fragment:04057"
a 46587 c 48574 g 46393 t 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-415K20"
/clone_lib="RPCI-11.2"
1. .128065
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:03248
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                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47.2; DB Pred. No. 0.32;
                                                  151076 bp
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dq 001
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                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 others
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 189409;
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                  HTG 21-JAN-2002
, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         0
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SOURCE
ORGANISM
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Homi
Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (bases 1 to 151076)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-682B13
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Center clone name: 682_B_13
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                                                                                                                                                                                                                       Submitted (21 MAR-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nlas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Dec 6, 2001 this sequence version replaced gi:13429999.

On Dec 6, 2001 this sequence version replaced gi:13429999.

Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTNZ.0, BLASTNZ.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nlh.gov/Dlast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against the Identified DNA Sequence with BLASTP2.0. ESTs represent the Identified DNA Sequence with BLASTP2.0.
                  the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 145120)
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is classified as a 'hypothetical' protein.
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C clone:P0452F10.
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The orientation of the sequence is from T7 to SP6 of the PAC clone. This sequence of P0452F10 clone has an overlap with P0485009 (DDBJ: AP001859) at the position 92,933 to 145,120 of 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(3049.
5211. .5279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MEEGKRIROVFGRVTGWSVSKTEDIFVVTVRKYLRTVTTGSNSI
NLVVVVDGKSAVRMPPVRAMRAIVLAAACTECLARTRN"
join(10963. 11280,12207. 12285,12396. 12531,13093. 13288,
13475. 13543,13695. 13834,14005. 14127,14970. 15162,
16452. 16614,17013. 17056,17279. 17369,18595. 18738,
18827. 18866,23823. 23963,24030. 24075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10459.
                                                                                        LCTREAMNVMQHQQKGGHVFNMDGAGSGGSSTPLTAVYGSTKCGLRQFQASLLKESRR
SKVGVHTASPGMVLTDLLLSGSSLRNKQMFNLICELPETVARTLVPRMRVVKGSGKAI
NYLTPPRILLALVTAMVRRGRWFDEEGRAVYAAEADRIRNWAESRARFSFTDAMEMYT
                                                                                                                                                                              GEEASSSPPPPTTAEARRRKGPLYKLKAAIQGLAGSRSAAAEAYGGEYQRAVEKAEE
IFFSVATQVGRYVITMMSSGVVLGVGFQLSGGDSQMTLIWYSMLGGVILGTMICAKS
VLEEHCKAGFRANVITGSPESYLQTIXELEENIQEGLSVAKKKOREILLHAKVYGTSC
DVCKPEDVKKLVNFAKDELGSIDIWINNAGTNKGFRPLVNFSDEDISQIVSTNLVGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          similar to Arabidopsis thaliana hypothetical protein F17N18.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(10963. .11280,12207. .12285,12396. .12531,13093. .1
13475. .13543,13695. .13834,14005. .14127,14970. .15162,
16452. .16614,17013. .17056,17279. .17369,18595. .18738,
18827. .18865,23823. .23963,24030. .24075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAPILVVYSSAVACASARLLLGRHARPCTAAPVYLSVAGSLVMILNPLDQYYYYY°
complement(join(9838. .9932,10020. .10126,10340. .10380,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5211. .5279)
/gene="P0452F10.1"
join(8115. .8396,9324.
/gene="P0452F10.2"
                            ENTWVSVFSLSVVCAFIILSSSVARLHRMLQPPIELKPCRVMILLDGEAGRSLHLVQT
MYGFLCASHFFNIAIIMYIHATARPVQIIPMWRGVHPEQWLMCLEVNDFFGFLTRLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="1"
WSHGGIHVVMYFISHDKCRREKGHSSRSNPPFTDAWDPPRSNATLTQVTVARNAPAII
                                                                                                                                                                                                                                                                                                      /protein_id="BAB78667.1"
/db_xref="GI:17385727"
/translation="MAAAAVVHLSVHGRLRRSPELHARPYHRPSLLRCRAFKQEADNG
                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB78665.1"
/db_xref="GI:17385725"
/translation="MPRRTPAAAAVHTTRRLSRLPLFSPSSTWERAEAAAADRAGVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(8115. .8396,9324. .9341)
/gene="P0452F10.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Rice myb-related
includes stop codon(s)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="contains EST AU064167(E4058)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="P0452F10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB78666.1"
/db_xref="GI:17385726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="P0452F10.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="P0452F10.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /pseudo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(3049. .3420,4142. .4504,4612. .4878,5066. .5206,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="P0452F10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lement(join(9838. .9932,10020. .10126,10340. .10380,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .3420,4142. .4504,4612. .4878,5066. .5206,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9341)
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CDS

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KKRHHHHHPPPPPPPHLLHYVGHPPPPPPPFKGDHYGGVVQMQQMGPPPPDHV
LKXVPSHPSPPPPHLLHYVGHPPPPPPPPFKGDHYGGVQMQQDKPPPPDHV
LKXVPSHPSPPPPPHLHYVGHPPPPPPPFKGDHYGGVMQQDKPPPPTTTEDLSA
LKXPSHPSPPPPPPPPHLHPYVGHPPPPPHLHTSRVHH
ATDGFSDANLLQQGGFCYVHKGYLPNGTEVAVKQLRDGSGQGEREFQAEVEIISRVHH
KHLVTLVGYCISGGKRLLVYEYVPNNTLELHHHGRGRPTMEMPTRLRIALGAAKGLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDARQIPETEMEMGSLKKDGDSNGTRDSQAS"
join(30710..30762,30889..30915,31041..31140,32690.
32922..33008,33095..33234,33611..33710)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYASSGQLTEKSDVFSFGVMLLELITGRRPVRSNQSQMDDSLVDWARPLMMRASDDGN
YDALVDPRLGQEYNGNEMARMIACAAACVRHSARRRPRMSQVVRALEGDVSLDDLNEG
VRPGHSRFLGSYNSNEYDTGHYNEDLKKFRKMAFGSGNLESSQQTQPTEFVPNRSVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(24964. .25375,26027. .26542,27087. .27173,27278. .27728. .27804,27960. .28107,28553. .28714,28954. .29274)
/gene="p0452r10.5"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(24964. .25375,26027. .26542,27087. .27173,27278. .27348,
27728. .27804,27960. .28107,28553. .28714,28954. .29274)
/gene="p0452E10.5"
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/protein_id="BAB78668.1"
/db_xref="GI:17385728"
/translation="MSSPSSPPPANQTATPPPANQTAAPPPASNNSSSPPAPGSLSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0452F10.6"
join(30710. .30762,30889. .30915,31041. .31140,32690. .32836,
32922. .33008,33095. .33234,33611. .33710)
/gene="P0452F10.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHEDCHPKIIHRDIKSANILLDARFEAKVADFGLAKLTSDNNTHVSTRVMGTFGYLAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAMRARDAAFASRARVRMAERLIYGRDMVFAPYGEFWRQARRVSVLHLLSPRRIASFR
GYREQEVAALLDRVRRRCGVRGGGETVNLSDLLMSYANGVISRAAFGDGAYGLDGDEG
GEKLBELFANFEALLGTATVGEFVPWLAWVDKLMGLDAKAARISAELDGLLERVIADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGFNVEAAFECIARNAIKNEPEEEIIFLIQLMLEVLEGNSARQAVNARRYGTSDIAS"
join(34853...35857,36458...37129)
//ence"P0452F10.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="masrrmllkylilgdsgygktslmnqyynkkfsnqykatigad
flikeyqiddrlftlqiwdiagqerfqslgyafyrgadccylyydynytksfeblnsw
reefliqaspsdpenfpfyylgnkidydggnsrtysekkakawcaskgnipyfetsak
                                                                                                                                                                                                                                                                                                                                                                        LYHFDWELFEHADGAAAATAARLDMGELFGLSMRMKTTLNLVAKPWSSDV"
Join (39698. 40690, 40829. 40832, 42030. 42769)
/gene="p0452F10.8"
Join (39698. 40690, 40829. 40832, 42030. 42769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRLLRAVVKETLRLHAPVPLLVPRETVEDTELLGYRVPARTRVIINVWAIGRDAAAWG
DRAEEFVPERWLDGGGEEVEYAAQLGQDFRFVPFGAGRRGCPGAGFAAPSIELALTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MELSSSLAAVLHSPLFLLAALLLLPVFTLLSFSSAKKPGDGGGW
RLPLPPSPRGVPFLGHLPLLGSLPHRKLRSMAEAHGPVMLLWFGRVPTVVASSAASAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="BAB78670.1"
/db_xref="GI:17385730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(34853. .35857,36458. .37129)
/gene="P0452F10.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="RAS-related GTP-binding protein Rab7 family"
/protein_id="BAB78669.1"
/db_xref="GI:17385729"
                                                                            EVMRTRDLAFASRPRVRMSERLFYGRDMAFAPYGEFWRQARRVTVLHLLSPRRVLSFR
GVREQEVAALLDRVRRRCGGGGETVNLSDLLMSYAHGVISRAAFGHGGAHGFDGDEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RERRRLSQPDGGDGDGDGDDENVDHRDFVDVLLDVSEVEEGAGAGEVLLFDTVAIKAII
LDMIAAATDTTFTTLEWAMAELINHPPVMRKLQCEIRAAVGVPGASGGAEVTEDHLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains EST C98812(E3123)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="contains ESTs AU056253(S20425),AU056254(S20425)"
                         EKLRKLFADFEGLLGTMTVGEFVPWLAWVDKLTGLDAKVARTSAAMDGLLERVIADHR
ERRRSRGQAVGDGEADADHRDFVDVMLDVSEAEEGAGAGAGGVLFDTVAIKAVILSKK
                                                                                                                               /db_xref="GI:17385731"
/translation="MELSSLAALLHSPLLLAVLLLVFSWLIVSSTKKRPPPPPCGDGGR
RLPLPPSPPGVPLLGHLPLLGTLPHRKLRSNAEAHGPVMLLRLGRVPAVVASSAAAAE
                                                                                                                                                                                                                                                                                                                     /gene="P0452F10.8"
/note="contains EST C98812(E3123)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
VPRVTCMNERFIEQDMMAAGTDSSFTTTEWVMAELINHPRVMRKLQDEIRAVVGTSSA
                                                                                                                                                                                                               /protein_id="BAB78671.1"
                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative cytochrome P-450LXXIA1 (cyp71A1)
                                                                                                                                                                                                                                                                     putative cytochrome P-450LXXIA1 (cyp71A1)
                                                                                                                                                                                                                                                                                                                                                       .40690,40829. .40832,42030.
2F10.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .32836,
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AUTHORS
TITLE
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VERSION
KEYWORDS
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ORIGIN
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                                       524
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Db 134344 TGCCGGCCCATTTTCACTTCCAAACTTTCGACCGTGAGATTCCTCCTCATGCTTGGAAAT 134403
                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                         464 tctgctctctatctcggattttccatgaccagaaaaaatgtgatgaacacaaagctagtt 523
                                                                                                                                                       404 aatgcgagcatttctccataagagggtatgttgctcttcttcagaagaaggatccaaaat 463
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WWTNHAKRGATMCWYWYWTGTNRRWCMRTYAMRTWYTRSNANWSCATKBMWWTMKWYATK 1032
                                                         YRTAWYAMWCAWRNINMWCATIGYAKSCATINAMWYATTRWAAYAAAKWARWAGINMRMY 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1141 bp
Sequence 22 from Patent W00111061.
AX083744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regulation of embryonic transcription patent: WO 0111061-A 22 15-FEB-2001; UNIVERSITY OF BRITISH COLUMBIA (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kunst, L. and Clemens, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       artificial sequence.
1 (bases 1 to 1141)
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/gene="P0452F10.9"
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/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                      YWYWRYDYWCAMCWMNAKAKVRTAMKHMWYYTDRYVSANNTGVRWMMMRWCMW
                                                                                                                                                                                                                                                                                                                       cagaaattataaatgctaaccaggttgaggattctagaagtgacgaagttcat 1416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtgagcagatctgcaatgagccatgtgaagaagttgttctcamaagaagctccaaatcta 1243
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 93100)
                                                                                                                                                                              Human DNA sequence
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                                                                      Homo sapiens
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66184 TACATCTCTTTTTGCCACATCCATGCTAACATCTATTATTTTTTGATTTTTAAATTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                             66244 CCATTCTTGCAGGAGTAAGGTGGTGTCTCATTGTGGTTCTAATTTGCATTTCCCTGATAA
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone, as we submit sequence subhission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aacttctagcaggaaccagatggagtctcaacttcataattctcagtatgcacataatca
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                                                                                                                                                                                                                                                                                                                                                               attcgaagacttat 2992
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                                                                                                                                                                                                                                                                                                      AATTGTCTATTTAT
                                           Homo sapiens chromosome 11 clone SEQUENCE, 3 unordered pieces. AC087825
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AC087825.2 GI:14192972
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RP1-220G17 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-76K20 is at 91101 in this seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP1-220G17 from the library RPCI-1 constructed by the group of Pieter de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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/clone="RP1-220G17"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                      66377
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Pred. No. 1;
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                                                                                                                    RP1-220G17
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SOURCE
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Marquis, N., Matthews, C., McCarthy, M., McBwan, P., McRernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V.,
Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K.,
Phunkhang, P., Plerre, N., Pollara, V., Raymond, C., Retta, R.,
Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (28-JAN-2001) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On May 24, 2001 this sequence version replaced gi:12584323. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S. Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Fitzhugh, W., Gand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRoque, K., Lamazares, R., Landers, T., Johnson, R., Landers, R., Landers, R., Landers, T., Johnson, R., Landers, 
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1 (bases 1 to 114980)

Birren,B., Linton,L., Nusbaum,C. a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.
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Insert size: 114780; sum-of-contigs
Quality coverage: 10.3 in Q20 bases; agarose-fp
Quality coverage: 10.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 114348 bases at least Q40 Consensus quality: 114583 bases at least Q30 Consensus quality: 114709 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: 220_G_17
------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
                                                                                                                                                   1 5011: contig of 5011 bp in length
5012 5111: gap of 100 bp
5112 73744: contig of 68633 bp in length
73745 73844: gap of 100 bp
73845 114980: contig of 41136 bp in length
                                                                                                  Location/Qualifiers
/organism≔"Homo sapiens"
                                                      .114980
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e RP1-220G17
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TITLE
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Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theoretirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., )
                                                                                                                                                                                                                 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McSwan, P., McGurk, A., McKernan, K., McKernan, K., McKernan, K., Marquis, N., McSwan, P., McGurk, A., McKernan, K., McKernan, K
                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
                                                                                                            McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren,B., Linton,L., Nusbaum,C. and Lander,E
Homo sapiens, clone RP11-15F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens clone RP11-15F4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Mammalia;
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(bases 1 to 158392)
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/note="assembly_fragment
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/chromosome="11"
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Pred. No. 1.1;
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1-15F4, WORKING DRAFT SEQUENCE, 2 ordered
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                                   gtacaaaggatcaaccagcacatcatatggcagtaacctgaatggaaagattccattgac 2978
                                                                                                                                                                                           TACATCTCTTTTTGCCACATCCATGCTAACATCTATTATTTTTGATTTTTAAATTATGG
  CCATTCTTGCAGGAGTAAGGTGGTGTCTCATTGTGGTTCTAATTTGCATTTCCCTGATAA
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 163000; agarose-fp
Insert size: 158292; sum-of-contigs
Quality coverage: 13.8 in Q20 bases; agarose-fp
Quality coverage: 14.2 in Q20 b.
NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  48372 a
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1 39274: contig of 39274 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L3455
Center clone name: 15_F_4
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/db_xref="taxon:9606"
/clone="RP11-15F4"
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L. .39274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (01-DEC-1993) Hansi J. Dean, Virology Swine Research Unit, U.S. Department of Agriculture, Ames, IA 50010, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHIUL45A 3400 bp DNA linear VRL 28-OCT-1994 Pseudorabies virus helicase (UL5) and UL4 genes, complete cds. L20708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 202 (2), 962-967 (1994)
94303212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 3400)
Dean, H.J. and Cheung, A.K.
Identification of the pseudorables virus UL4 and UL5 (helicase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudorabies virus (strain Indiana-Funkhauser) DNA
Pseudorabies virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L20708.1 GI:431464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dean, H.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 3400)
                       /protein_id="AAA50987.1"
/db_xref="GI:431466"
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CDALAPGRVTIQHGPVITVLAVDGEPERCSYVFARTWPAAPEGALVMPFSTWSCAERS
RRLRGPAGGLLATLVAERALHVTITAYRPDVLRDALREARILE"
a 1241 c 1160 g 497 t
                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLAWEKSLAAADNPVDIEALELPFAAYLISGNAGSGKSTCIQTLNETMDCVVITGSTR
VAAQNVYAKLSAAYSSRYVNIT FQEFGFRGHIVQAAQLGRYSVACPTSPPTVRELQKRD
LVYYWEVLQDISRRVLAGSHEEFARLERLTIGRAAEHLAFACHGSLPAFARSNIV
IDEAGLLGRHLLTAVVYCWWLLNAAVDTTQYAARARPVLVCYGSPTQTDSLESRFEHA
RQLCRVRASENLLTYLITNRALREYTDLSRNWAIFINNKRCQEYEFGELMKALEYGLP
LTDEHLRLUDSEVVPERYINPANLQGWTRLYSSHREVSAYMSRLHAHLKVAGDAQFV
VFTLPAYTIVRTAAFDXYREATQOPHLTLDRHLAANAGRITNYSGSROQDAAALRCEA
RAQGGVVLARCEVTYVLNGQVAVTTRLKKLVIGFSGFTEAFAAVLRDAFVHAQGGSA
RAQGGVLARCEVTYVNFLQFPGLAFEAVVAAYRRLAAVVRAAALRVPEEHFDFSG
EYTYRFLSSLLESGMIAFYNFLQFPGLAFEAVVAAYRRLAAVVRAAALRVPEEHFDFSG
AAAPAAPAGFGGAADDDDDLFAALSENMLDMLYCHYDFARPETTSEYYAQFLMKKTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="UL5"
217. .2718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pseudorabies virus"
/strain="Indiana-Funkhauser"
/db_xref="taxon:10345"
                                                                                                                                                                                                                                                                                                                                             LRMNMNPLREEPERDNGISEHILAALRDGAVHIVY"
                                                                                                                                                                                                                                                                                                                                                                                            THATAPAFAEELARRKLHAGTAELLASLDTPRVVLRDQSGFLSILNVNLSDFVESLDD
                                                                                                                                                                                                                                                                                                                                                                                                                     ADRYAALSELFGPAFARAPFETHVDSVSVRGCEVFVGGLRGALLSTALQTDSYTLVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="helicase"
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                                                                                                                                                                                           /function="unknown"
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="UL5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                      codon_start•1/
                                                                                                                                                                                                                                              'gene="UL4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virus was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    passed in Madin-Darby bovine kidney
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REFERENCE
AUTHORS
TITLE
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ACCESSION
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AC107868/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FOCUS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 ctcgtggtggaactggtgctgtagcgccagtgttggagctgacagcgacgcctcgtcagg 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 tggagattgttgcagtagatcaggagggaggtcgtgttgttgggacgaactgtatgcttg 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602 CCGAACTCCTGGAAGATGGTGTTCACGTAGCGGCTCGA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 atgcagccgctgaagctggtgtagacggaaccggcacaa 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           662 CTCGTGGGGCACGCGTAGCTGTAGCGCCCGAGCTGCGCCTGCACGTGGTTCCCGCGGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hılme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
MacGonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McCwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., McOl, R., Norbu, C.,
Morman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Triglilo, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity
87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhqalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitchugh,W., Gage,D., Galagan,J., Gardyna,S., Colde, P., Collymore, A., Cook, P., Collymo, R., Collymo, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 65478)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Misculus, clone RP23-405A17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-JAN-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC107868.1 GI:18308571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
NOTE: This record contains 81 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 65478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                        Center project Information Center project name: L20687 Center clone name: 405_A_17
                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTGS_PHASE0.
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                                                                                                                                                                                                                                                               http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                       Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44.4;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                          for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overlap relationships among clones to be deduced However, it should not be assumed that this clone
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                                                                                                                                          20903 21636: contig of 734 bp i
21637 22463: gap of 100 bp i
21637 22462: contig of 726 bp i
22463 22562: gap of 100 bp i
23302 23301: contig of 739 bp ir
23302 23401: gap of 100 bp ir
23402 24081: contig of 680 bp in
24082 24181: gap of
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19182 19281: gap of
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100 bp
100 bp
100 gap of 100 bp
110 3891: contig of 682 bp
12 3991: gap of 100
12 4701: contig of 82 bp
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61 11257: contig of 712 bp 1
61 11357: gap of 100 bp 1
61 1273: contig of 716 bp 1
74 12173: gap of 100 bp 1
74 12890: contig of 717 bp 1
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82 19996; contig of 715 bp
97 20096; gap of 100 bp
97 20802; contig of 706 bp
03 20902; gap of 100 bp
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1 6440: gap of 100
1 7172: contin
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8105: gap of 100 by
8832: contig of 727
8932: gap of 100 by
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101: gap of 100 bp

5520: contig of 719 k

20: gap of 100 bp
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17: gap of 100 bp 109: contin of 100 bp 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: contin of 109: co
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13570: contig of 580 bp
70: gap of 100 bp
14394: contig of 724 bp
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21 36320: gap of 100 bp
21 37019: contig of 699 bp in 16
20 37119: gap of 100 bp
20 37831: contig of 712 bp in 16
20 37831: gap of 100 bp
32 38591: contig of 600 bp in 16
92 38691: gap of 100 bp
92 38691: gap of 100 bp
93 38691: gap of 100 bp
96 39379: contig of 688 bp in 16
97 38691: gap of 100 bp
98 39479: gap of 100 bp
80 40189: contig of 710 bp in 16
80 40189: gap of 100 bp
80 40189: gap of 100 bp
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3239: contig o

3239: gap of

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                                                              48373: contig of 738 bp 11
48204: contig of 731 bp 11
19304: gap of 100 bp
50024: contig of 720 bp 11
10124: gap of 100 bp 50
50806: contig of 682 bp 11
50906: gap of 100 bp 51
1708: gap of 100 bp 51
17108: gap of 100 bp 51
17108: gap of 100 bp 52
52517: contig of 709 bp 11
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41022: C
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.49: gap of
28145: 7
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45925: contig of 731 bp 1
6025: gap of 100 bp
46761: contig of 736 bp 1
6861: gap of 100 bp
47535: contig of 674 bp 1
7635: gap of 100 bp
48373: contig of 738 bp 1
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4738: gap of 100 bp
35425: contig of 687 b
5525: gap of 100 bp
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3056: gap of
29789: contig c
54064: contig
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54877: contig
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74: contig of 732 bp in
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:: EmBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20

This sequence is the entire insert of clone RP5-897D18 The true left end of clone RP11-4603 is at 76409 in this sequence. The true right end of clone RP11-4603 is at 76409 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence. The true right end of clone RP4-539E24 is at 40325 in this sequence at 11 sequence was finished as follows unless otherwise noted: all end in the sequence at 11 sequencing problems, such assembly was confirmed by restriction dieset pp5-807D18 is from the sequence of more than one M13 subclone; and the from the sequence in the from the sequence of the form
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AL133232
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On Jun 21, 2000 this sequence version replaced gi:8574104.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                8410. .8697
/note="AluJb repeat: matches 1.
8708. .8867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6199
                                                                                                                                                                                                                                                                                 9448. 9450
/note-"Tandem repeat. Forced join. Approximately 350 bases missing according to restriction digest data"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5332. .5406
/note="L2 repeat: matches 2617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="Alu repeat: matches 1. .40 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP5-897D18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5588. .6734
/note="L2_repeat: matches 1990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1311. .4414
/note="MIR repeat: matches 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3963. .4284
/note="AluSp repeat: matches 1.
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                                                                                                                                                                                              /note="AluJb repeat: matches 1.
11021. .11313
                                                                                                                                                                                                                                               /note="MIR repeat: matches 51. .155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="MIR repeat: matches 65. .143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MLT1D repeat: matches 12.
3326. .8397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5985. .7285
/note="AluJo repeat: matches 1.
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.735. .2754
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                                                                  note="L1MD2 repeat: matches 6052. .6326 of consensus"
                                                                                                    note="Alux repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                           3. .8939
te-"MLT1J repeat: matches 269. .313 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                               8. .8867
te="MLT1J repeat: matches 48.
                                                                                                                                                                            te="AluSx repeat: matches 1.
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                              repeat: matches
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                                31.
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12727. .13033
.note="Aligx repeat: matches 1. .308 of c
                                         ..... repeat: matches 1. .224 of complement(join(<28867. .28921,29503. ./gene="dJ897D18.1"
                                                                                                                                                                                  /note="Alux repeat: matches 1. 26737. .26910
                                                                                                            /note="AluSg repeat: matches 1.
27855. .28078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1MD2 repeat: matches 5502. .5934 of consensus"
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17944. .17994
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/note="AluSq repeat:
25996. .26231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .8047. .18078
'note="16 copies 2 mer tt 84% conserved"
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                                                                                                                                                                                                                                                        note="L1MC3 repeat: matches 7160. .7451 of consensus"
%370. .26427
                                                                                                                                                                                                                                                                                                                                            note="LIMC3 repeat: matches 7451. .7735 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                note="Alusg/x repeat: matches 92. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        3794. .24101
'note="AluJb repeat: matches 1.
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22190. .22419
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note="L2_repeat: matches 2130.
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note="MER45B repeat: matches 926. .1039 of consensus"
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                   /evidence=not_experimental
                                       note="match:
                                                                                                                                                               'note="AluSc repeat: matches
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57. .17436
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e="L2 repeat: matches 2323. .2750 of consensus"
9. .14778
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                                      ESTS: Em:AI377332*
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                                                                                                                                                                   135.
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complement(j0in(28867. .28921,29503. .29930))
/gene="dJ897D18.1"
30614. .30718
/note="MIR repeat: matches 73. .179 of consensus"
30788. .30845
30847 30847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30847. .30941
/note="AluJo/FRAM repeat: matches 192. .286 of consensus"
30946. .31076
/note="MIR repeat: matches 106. .240 of consensus"
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Search completed: September 16, 2002, 20:36:45 Job time: 15337 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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(without alignments)
11866.626 Million cell updates/sec
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Drosophila melanog
Arabidopsis thalia
DNA encoding novel
DNA encoding novel
S. epidermidis gen
Human wild-type pr
Human cancer assoc
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AAI18167	AAK37335	AAK11566	ABA30385	ABA63135	AAI00573	AAI31897	AAI10643	AAK26014	AAK00565	ABA22091	ABA52290	AAI07733	AAI56167	AAI47330	AAI27301	AAI22038	AAK50216	AAK41287	AAK24165	AAK15554	ABA40197	ABA34204	ABA75585	ABA67114	ABA49199	AAH48024	AAA29550	AAI94740	ABL32504	AAV63196	AAZ38223	AAS92080	AAH54703	ABL32775	ABL34624
Probe #8100 for ge	Human bone marrow	Human brain expres	Probe #8851 for ge	foets			Probe #576 for gen	Human bone marrow	Human brain expres	: #557 fc	Human foetal liver	Probe #7724 used t	#24853	used	#17234	#11971 for	bone	bone n	brain	brain expre	#18663 for	#12670	foetal	foetal	east cell	Internal control B	٥	neurobl	immune sys	cDNA from clone fp	Human S184L mutant	DNA encoding novel	۳.	Human immune syste	Human metastasis a

ALIGNMENTS

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RESULT 1
ABL06815/c
               WPI; 2001-656860/75.
P-PSDB; ABB62712.
                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ ID NO 14927.
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                                                                            23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                          WO200171042-A2.
                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                           ABL06815 standard; cDNA; 1788
                                                                                                       23-MAR-2001; 2001WO-US09231.
                                                                                                                        27-SEP-2001.
                                         Venter JC,
                                                          (PEKE ) PE CORP NY
                                         Adams M,
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New isolated nucleic acid detection reagent for detecting 1000 or more

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Best Local Similarity
Matches 130; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1788
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
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                                                                          CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  developmental biology; cell signalling; insecticide;
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food supplement;
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99US-0160815.
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99US-0160770.
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99US-0159637
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11-OCT-2001.

WO200175067-A2

30-MAR-2001; 2001WO-US08631.

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PPN XXX XXX PPN PN PN XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for identifying expressed genes. (I) is useful in gene therapy techniques (II) (II) or to treat disease states involving (III). (II) is useful in generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical cisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disponsitics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS6419-AAS94564 represent novel human classification, but was obtained in electronic format directly from WIPO as the viro introduction obtained in electronic format directly from WIPO as the viro introduction of the inventions.
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                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                             DNA encoding novel human diagnostic protein #11729
                                                                                                                                                                                                                                  13-FEB-2002
                                                                                                                                                                                                                                                                                                     AAS75925 standard; cDNA; 2456 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 246 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 26483; 103pp; English.
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC consists are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polypucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations composities, forensics, gene mapping, identification of mutations composities, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution, but was obtained in electronic format directly from WIPO
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23-AUG-2000;
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                                                                                                                                                                                                    AAH54196;
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              WO200134809-A2
                                              Staphylococcus epidermidis
                                                                                             Staphylococcus
                                                                                                                               S. epidermidis
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2000US-0649167.
                                                                             us epidermidis 
endocarditis;
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                                                                                                                               genomic polynucleotide sequence SEQ ID NO:3560
                                                                                                                                                                                                                                    DNA;
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s useful as hybridisation probes
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                                                                                               infection; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC (II), given in AAG81454 to AAB33120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used CC (I) and (II) can have antibacterial activity and therefore can be used CC in vaccination. The nucleic acids (I) may be used to produce the CC s. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and therefore identify compounds that may be used for the cativity and the present invention. AAH53971 to AAH55091 to AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

CC AAH55098 represent invention specifically claims all the polynucleotide sequences given in the disclosure for SEQ ID NO:4454 so even compounds that the present for SEQ ID NO:4455 to 4472, compounds that the present 
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Matches 105
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                                                                                                                                                                            AAZ32967 standard;
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Human wild-type protein kinase MKK4 gene fragment E

MKK4; mitogen activated protein kinase; MAPK; MAPK pathway;

mutation;

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CC also involved in suppressing a variety of tumours. MKK4 is a dual context and involved in suppressing a variety of tumours. MKK4 is a dual context and page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of the page of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Columns 71-74; 63pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phorylation; Jun kinase; JNK; p38; tumour; suppressor; of heterozygosity; LOH; cancer; detection; diagnosis; prognosis; st cancer; pancreatic cancer; colorectal cancer; testicular cance screening; gene therapy; protein replacement therapy; mimetic; d
   mutation
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Best Local Similarity
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                                             AAA09310-20 are novel genes isolated by SEREX screening from a renal cancer cell line 1973/10.4. The genes encode cancer associated antigen precursors. These gene products are useful in methods for preventing, diagnosing and/or treating disorders, especially cancer, associated with abnormal expression of human cancer associated antigens. The method
comprises contacting a sample from a subject with an agent that specifically binds to the nucleic acid molecule or expression product (or fragment) complexed with a human leukocyte antigen (HLA) molecule and determining the interaction between the agent and the nucleic acid
                                                                                                                     Claim 57; Page
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(pos:59..64, aa:Gly)
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Best Local
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                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system as genes which are modified by the methylation of cytosines. The seq can be used in the diagnosis and treatment of immune system disor including eye diseases such as retinopathy, neovascular glaucoma
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degeneration,
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No. 0.
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  anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                      German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                          antiasthmatic;
                                                                                 gene, us
                                                                                                                                                                                                                                                                                       anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      686;
                 The sequences em disorders,
                                                                                                                                                                                                                                                                       disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                    associated
 myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT
ABL34624
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Best Local :
Matches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                        WPI;
                                                                                                                                           01ek
                                                                                                                                                                                                                                                                                                     Metastasis associated cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia, Alzheimer's disease, AIDS, rheumatoid arthritis, psoriasis and in diseases. The present sequence is a go
                                                                 Claim 1;
                                                                                   also
                                                                                           New nucleic acid derived from chemically treated metastasis useful for diagnosis of cancers by analysis of cytosine meti
                                                                                                                                                                                                                             06-APR-2001;
                                                                                                                                                                                                                                                                  WO200177376-A2
                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                      ABL34624;
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                                                                                                                                                                                                                                                18-OCT-2001
                                                                                                                                                           (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tgtgtgtttgtgtgtgtttttgtaggggttcgttgtagttgttttgggtgtttggtt 14884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgattgattgtcttctgtgatatatccagagctcgtgttttgtggttttgtggtt119
                                                                                   for
                                                                                                                         2002-010922/01.
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                                                                                                                                                                                                                                                                                                                                 metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity 51.0
116; Conservative
                                                                                                                                                            EPIGENOMICS
                                                                 SEQ
                                                                                   treatment
                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15518
                                                                                                                                          Piepenbrock
                                                                                                                                                                              ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
                                                                                                                                                                                                                             2001WO-EP03970
                                                                 ID NO 177;
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                  associated
                                                                                                                                                                                                                                                                                                                                                                                         DNA; 15518
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                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                    gene;
                                                               23pp +
                                                                                                                                            Berlin
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; Pred. No. 4.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 C; 4183 G;
                                                                                                                                                                                                                                                                                                     cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                 Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                  SEQ
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                                                                                                                                                                                                                                                                                                               gene therapy; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 15518;
                                                                                                                                                                                                                                                                                                                                                                                                                                       15048
                                                                                                                                                                                                                                                                                                                                                                                                                                                         284
                                                                                           methylation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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The present invention provides a number of human metastasis associated genes which are modified by cytosine methylation. The sequences can be used in the diagnosis and treatment of cancer. The present sequence is one of the genes of the invention.

Sequence

15518

BP;

3047

362

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4183

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7926

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RESULT 11
ABL32775/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL32775 standard; DNA;
                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                  WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                     WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
            macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                             Claim 1;
                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgtgtgtttgtgttgtgtgttttgtaggggttcgttgtagttgttttgggtgttttggtt 14884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gttttagtttttgttttaggttagttggaggggagttttatggg 15048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tatggagattgttgcagtagatcaggagggagctcgtgttgttgg 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttgagttgtgcctcggctgtgctggctgtgttgattctctcctcgtcgtggtgatcga 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgattgattgtcttctgtgatatatccagagctcgtgttttgtgggtttgtggtttgtggt 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system disease; cytosine methylation; antiasthmatic;
zeriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                          methylation
                                                                                                                                                                                                                                                             Piepenbrock C,
                                                                                                                                             SEQ ID NO 748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                          ĀG
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                                                                                                                                             32pp + Sequence Listing; German
                                                                                                                                                                                                                                                             Berlin
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Pred. No. 4.
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                                                                                                                                                                                         gene, us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15518;
                                                      acute myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                       useful
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY
       CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. CC (II) and (II) can have antibacterial activity and therefore can be used CC (I) and containing the nucleic acids (I) may be used to produce the CC containing them which are used to produce hosts cells which express the CC containing them which are used to produce hosts cells which express the CC used to vaccinate subjects and to raise antibodies against the bacteria. CC used to vaccinate subjects and to raise antibodies against the bacteria. CC The polypeptides may also be used to assay for other inhibitors of their cativity and therefore identify compounds that may be used for the cC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA CC AAH55098 represent oligonucleotide sequences and primers which are used CC in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15122 BP; 3782 A; 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S. epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH54703 standard; DNA; 3257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6515 AATAAAC 6509
                                                                                                                                                                                                                                 Claim 8; Page 1752-1753; 2188pp; English.
                                                                                                                                                                                                                                                                          Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                               Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis
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                                                                                                                                                                                                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for vaccinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 50.8
95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic polynucleotide sequence SEQ ID NO:4067
                                                                                                                                                                                                                                                                                                                                                                                      99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%;
                                                                                                                                                                                                                                                           polypeptides from Staphylococcus epidermidis, against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred.
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No. 5.
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                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000;
23-AUG-2000;
                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3257
                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
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                                                                                                                                                                                                                                                                                                                                                          2001-639362/73.
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96; Conser
                                                                                                                                                                                                                                                                                                                                   ABG27893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYSEQ
                                                                                                                                                   SEQ ID No 27884; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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2000US-0649167
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Pred. No. 2
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  expressed sequence tags
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CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fig. in the product of the polypublished pct_sequences.
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                          13-JUN-1997;
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                                                     23-NOV-1999
                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                    Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                            loss of hetero;
breast cancer;
                                                                                                                                                                                                                                                                                                                     somatic; signal transduction; apoptosis; stress; cytokine;
phosphorylation; Jun kinase; JNK; p38; tumour; suppressor;
                                                                                                                                                                                                                                                                                                                                                                               Human S184L mutant protein kinase MKK4 gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ38223;
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                                                                                US5989885-A
                                                                                                                                                                                                                                                                                                                                                   MKK4; mitogen activated protein kinase;
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79; Conserv
                                                                                                                                                                                                                                                                                            heterozygosity; LOH; cancer; detection; diagnosis; prognosis; cancer; pancreatic cancer; colorectal cancer; testicular cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           (first
                           97US-0874186
                                                                                                                                                                /*tag= a
248..367
                                                                                                                                                                                                                                                                             gene therapy;
                                                                                                                          /note= "MKK4
368..2167
                                                                                                                                                                                                         Location/Qualifiers
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Pred. No. 1.2;
0; Mismatches
                                                                                                                                       mutant
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No. 1
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                                                                                                                                                                                                                                                                                                                                                   MAPK; MAPK pathway;
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                                                                                                                                                                                                                                                                               mimetic;
                                                                                                                                                                                                                                                                                                                         mutant;
                                                                                                                                                                                                                                                                                                                                     induction;
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                                                                                                                                                                                                                                                                                                                                                   mutation;
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10-JAN-1997;

97US-0782482

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RESULT 1
AAV63196
ID AAV6
                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a fragment of the gene encoding human $184L CC mutant protein kinase, MKK4, which includes exon E. Exon E contains CC a base substitution of T for C at base 285, which changes a Ser codon CC (TCG) to a Leu codon (TTG). MKK4 (also known as JNKK1 and SEK1) may be C2 involved in a MAPK (mitogen-activated protein kinase) pathway for the CC signal transduction of cytokine-induced and stress-induced apoptosis. CC MKK4 is also involved in suppressing a variety of tumours. MKK4 is a dual CC specific kinase that activates Jun kinases (JNKs) and p38 (a MAPK) but CC on the conine and tyrosine and then go on to activate proteins further CC deletions of the JNK and p38 MAPKs are activated via dual phosphorylation CC on threonine and tyrosine and then go on to activate proteins further CC deletions office involve loss of a single allele, which are a subgroup confidency good of MAPKs. The JNK and p38 MAPKs are activated via dual phosphorylation CC deletions office involve loss of a single allele, which are a subgroup confidency good of morfunctional, either because of a pre-existing inherited mutation, or because of a secondary sporadic mutation. Alternatively, the deletion cC deletions are relatively small in size, probably due to the proximity of cessential genes. Sequences derived from the MKK4 gene can be used to diagnose of a pre-disposition to breast, pancreatic, cc colorectal and testicular cancers, as specific MKX4 mutations have been found in cell lines derived from such tumours. MKX4 oligonucleotides care useful for the detection of the mucleotide sequence of a particular cancer therapy. MKX4 gene can be used to care useful for the detection of the microside sequence of a particular cancer therapy. TKX4 gene therapy protein midetics that reconstitute the function of the MKX4 protein may be used for therapy of human cancers which result cof the MKX4 protein may be used for therapy of human cancers which result cof the MKX4 gene the function of the MKX4 gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skolnick MH, Perry WL,
AAV63196 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a mutation in the MKK4 gene.
This sequence is not shown in the MKK4 gene fragment E shown
                                                                                               ataagttttacaaatatgtatatagtgt 318
                                                                                                                                   gtaattaccataaggaggtttatagtgt 3757
                                                                                                                                                                                                tattgtatttccattttaagtaaaggcaaggtgatatttaagatgtataagaataacaga 230
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Best Local Similarity 47.4

Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                          haematopolesis regulating activity, tissue growth activity, activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity or other activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agostino I
Racie LA,
                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a secreted protein. The nucleic acid sequence is isolated from a human adult placenta cDNA library using probe AAV63206. The polypeptide may have biological activities such e.g. nutritional activity, immune stimulating or suppressing activities.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; immune stimulating;
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                                                                       1607
                                                                                                                                                                                                                                                                                   Sequence 2522 BP; 740 A; 577 C; 637 G; 565 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 31; Pages 86-88; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adult brain, adult blood and placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide(s) and secreted proteins from human cDNA libraries prepared from adult testes.
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28-MAR-1997;
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                                                         gaaaaaagaaagaactggaagtgtgcatcacacagttgctcatccagctgggaatttga
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Treacy M;
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Search completed: September 16, 2002, 20:19:54 Job time: 12101 sec

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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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                                                  STRANDENNESS: SING-
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-Fls
JS-08-232-463-14
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Patent No. 5989885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Perry III, William L.
APPLICANT: Skolnick, Mark H.
TITLE OF INVENTION: SPECIFIC MUTAT
TITLE OF INVENTION: 4 (MKK4) IN HU
TITLE OF INVENTION: SUPPRESSOR IN
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/782,482
FILING DATE: 10-JAN-1997
FILING DATE: 10-JAN-1907
ANDRES/AGENT IMPORMATION:
ANDRES/AGENT IMPORMATION:
                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Teng, David H-F.
APPLICANT: Tavtigian, Sean V.
                                                                                                                                                                                                                                                                                           CITY: Washington STATE: DC
                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                           STREET:
                NAME: Saxe, Stephen A. REGISTRATION NUMBER: 3
                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Venable,
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                         U.S.A.
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4 (MKK4) IN HUMAN TUMOR CELL LINES IDENTIFY IT AS A TUMOR
                                                                                                                                                                                                                                                                                                                                                                                        SUPPRESSOR IN VARIOUS TYPES
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                  38,609
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Pred. No. 8.1e-09;
 24884-121392-01
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Best Local
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LOCATION:
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     tgttgggacgaactgtatgcttgctcgtggtggaactggtgctgtagcgccagtgttgga 338
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; SEQ ID NO 19
; LENGTH: 2190
; TYPE: DNA
; ORGANISM: Ashbya gossypii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2190)
US-09-625-188-19
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: NO. 6307037artis AG
APPLICANT: NO. 6307037artis AG
TITLE OF INVENTION: Fungal Tary
FILE REFERENCE: PB/5-31285P1
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09625188 Patent No. 6307037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-952-050: INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS: LENGTH: 2167 base pairs
                                                                              Query Match 1.0%;
Best Local Similarity 51.8%;
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/625,188
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 44
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1574 TGTTGTTGTGGTTGCTGTTGAGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC 1515
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                    totootogtogtggtgatogatatggagattgttgcagtagatcaggagggaggtcgtgt 278
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Similarity 54.7%;
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202-962-8300
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1..247
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                                                                               Score 37.6; DB pred. No. 0.33;
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                                                                   Mismatches
                                                                                                  DB 4;
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US-08-928-361B-4/c

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: LENGTH: 5163

: TYPE: DNA

: ORGANISM: Cryptosporidium parvum

US-08-700-651-1
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Best Local S
Matches 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CTYPTOSPORTIGHUM PARVUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(HY)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                GENERAL INFORMATION:
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                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1454 AGAGACTGTTGCTGCTGCTGCTGCTGCTGCTGCAGGTGCTG 1411
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nes 122; Conserv
                    STREET:
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NELSON, RICHARD, C.
   Palo Alto
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                 385 Sherman Avenue,
                                                                                                                                                  Petersen,
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                                                                               , CATOLYN
PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37.4; DB 3;
Pred. No. 0.72;
0; Mismatches 141;
                  JONES & BIKSA
e, Suite 6
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            Sequence 2, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: RELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PRO
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREAT
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(HY)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
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Best Local
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INFORMATION FOR SEQ ID NO:
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NAME: VERTY, Hana
REGISTRATION UNMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
EARLIER APPLICATION NUMBER: 08/415,751
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APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
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Local Similarity 46.4%;
nes 122; Conservative
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 5163 base pairs
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                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
DEDNESS: double
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                                                                                                PROTEINS,
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; ORGANISM: Cryptosporidium parvum
US-08-700-651-2
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US-08-928-361B-3/c
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LENGTH: 5318
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Best Local
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Petersen
TITLE OF INVENTION:
TITLE OF INVENTION:
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                 REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
APPLICATION NUMBER: US 60/026,062
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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CITY: P
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Local Similarity 46.4%;
hes 122; Conservative
                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 12-SEP-1997 CLASSIFICATION:
                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                               TELEPHONE:
                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                    385 Sherman Avenue,
                 650-324-1678
                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                  PETERS, VERNY, JONES & BIKSA
Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES INFECTIONS
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                                                                    480.76-1(HV)
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Pred. No. 0.74;
0; Mismatches 141;
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-928-361B-3
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US-08-676-967-2
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Best Local Sim
Matches 122;
; MOLECULE TYPE: US-08-676-967-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08676967 Patent No. 5747317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                      TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
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LENGTH: 5318 base pair
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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STATE: CA
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                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Science & Technology Law STREET: 268 Bush Street, Suite 3200
                                        STRANDEDNESS:
                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                             TOPOLOGY:
                                                                                                                                TELEPHONE:
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US-08-676-974-2
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                                                  Sequence 2, Application US/08676974 Patent No. 5770422
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Best Local Similarity
                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION UNMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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CITY: San Francisco
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                                STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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RESULT 10
US-09-098-487-2
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Best Local Similarity
Matches 116; Conserv
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APPLICANT: COLLIN
                                                                           TELEFAX: (415)343-4342 INFORMATION FOR SEQ ID NO:
                                                                                                                       REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCI
TELECOMMUNICATION INFORMATION:
TELEBULONE
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
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STRANDEDNESS:
                                     LENGTH:
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US-08-510-133A-32
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Best Local Similarity
Matches 116; Conserv
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GENERAL INFORMATION:
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                INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
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                                                                     APPLICATION NUMBER: US/08/510,133A
FILING DATE: 01-Aug-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28113/32863
TELECHMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accaaagateetaacecaatgtetggaaaggaaegtgateaggttgetgageagtgeaat 1146
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 60606-6402
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Alitalo, Kari
Joukov, Vladomir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARGAYGARGARGARAAYATHGARWSNAA 779
                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
LENGTH: 1140 base pairs
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; Pred. No. 0.81;
66; Mismatches 206;
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LOCATION: 37..1089
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-510-133A-32
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                                                                                                                                                                   TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Joukov, Vladimir TITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3: CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
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NAME: Gass, David A.
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FEATURE:
NAME/KEY:
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                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                        STRANDEDNESS:
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FEATURE:
                             LOCATION:
                                                                                           TOPOLOGY:
                                               NAME/KEY:
                                                                                                                                     LENGTH:
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77; Conserv
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                               CDS
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mat_peptide
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RESULT 14
US-08-999-811-3
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US-08-585-895-32
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LENGTH: 1525
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Best Local Similarity 53.1%;
Matches 77; Conservative
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Polynucelotides Encoding Vascular Endothelial Growth TITLE OF INVENTION: Factor 2
FILE REFERENCE: PF112D1
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hu, Jing-Shan
APPLICANT: Rosen, Craig
APPLICANT: Cao, Liang
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NAME/KEY: mat_peptide
LOCATION: (143)..(1120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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LOCATION: (71)..(142)
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LOCATION: (71)..(1120)
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                                                                    981 gaaagaagttccaccaccaaacatg 1005
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                                                                                        tatggtggtgaaagcaccagaaatg 1885
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                                                                                                                                        tabatcctggaaaatgtgcctgtgaatgtacagaaagtccacagaaatgcttgttaaaag 980
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                                                                                                                                                                                                                                                                              ; Score 36.2; DB; Pred. No. 0.7; 0; Mismatches
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US-08-999-811-3
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APPLICANT: HU, JING-SHA
APPLICANT: ROSEN, CRAIG
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VAS
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                Query Match 0.9
Best Local Similarity 53.1
Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
                        1861 tatggtggtgaaagcaccagaaatg 1885
                                                                                                                                                    1741 aatatgcataagacagatgtctgtcagcatgtatcagaaatctccacacagaggtgctca 1800
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LENGTH: 1526 base pairs
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APPLICATION NUMBER: US 0
FILING DATE: 06-JUN 1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US
FILING DATE: 8-MAR-1994
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981 GAAAGAAGTTCCACCACCAAACATG 1005
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ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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ROSEN, CRAIG A.
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RESULT 15
US-09-042-105-3
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Patent No. 6040157
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
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US-09-042-105-3
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Best Local Similarity 53.1%;
Matches 77; Conservative
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TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1526 base pairs
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
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APPLICATION NUMBER: TO BE ASSIGNED FILING DATE: 24-DEC-1997
CLASSIFICATION:
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PRIOR APPLICATION UNMBER: US 08/465,968
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
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NAME: ERIC K. STEFFE
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COUNTRY: C.
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1801 tcaaaggggaaaacagcgggtttgagtaaggggaaaacacattcagctgctagtaccaaa 1860
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STREET: 1100 NEW YORK AVENUE
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Search completed: September 16, 2002, 20:09:49 Job time: 11506 sec

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Maximum Match 100%
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen
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13360.877 Million cell update
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AW684844
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AL066286 Drosophil
AL063921 Drosophil
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AL066784 Drosophil
AL065923 Drosophil
AL059400 Drosophil
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AL071370 Drosophil
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BEIT7637 EST517582
AL071370 Drosophil
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1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.2	1.2	1.2	
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AQ744726	BE427089	AZ550256	BE427548	BE427036	CNS02CMF	CNS06TZ6	AW187871	AZ031624	C93179	AW727582	AZ267626	AG127302	AG135568	CNS00GPB	BG845969	CNS017ZT	BF242104	вн156851	CNS0075A	CNS018FL	AG130678	AI641313	AU060996	CNS006QP	CNS006ST	AG126399	AQ584620	
-	-	A2550256 ENTEV58TR	BE427548 PSR7168 I	BE427036 PSR6610 I	AL191328 Tetraodon	AL415192 T3 end of	AW187871 BNLGH1134	A2031624 RPCI-23-2	C93179 C93179 Dict	AW727582 GAEa001	AZ267626 RPCI-23-1	AG127302 Pan trogl	AG135568 Pan trogl	AL072375 Drosophil	BG845969 1024011G0	AL108707 Drosophil	_			AL109275 Drosophil	AG130678 Pan trogl	AI641313 fc13d05.y	AU060996 AU060996	AL065804 Drosophil	AL065880 Drosophil	AG126399 Pan trogl	AQ584620 RPCI-11-4	

ALIGNMENTS

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TITLE
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mays cDNA, mRNA sequence.
A1691520
A1691520.1 GI:4966664
EST.
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Zea mays
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Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
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Plate: 606020 row: C column:
Location/Qualifiers
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Maize ESTs from various cDNA libraries sequenced
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                                           /tissue_type="mixed"
/dev_stage="ear length from 0.5 cm -
/lab_host="%LOIR (Stratagene)"
/note="Organ: immature ear; Vector: p
                                                                                                                                  /organism="Zea mays"
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/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTATGGTACGGGTCAGCCTTCGACCAGTGGCAATGGGAGGACCATTCATCCGTTGGATA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCTCGTGAGGAAGGATATCTGTGTGACTANCAGAAAAGCAGCCGATTTCACTGTAATTA 184
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CNS0071A 895 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14B09 of RPCI-98 library from Drosophila melanogaster (fruit
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                   Conservative 115;
                                                                                                                                                                                                     /organism="Drosophila melanogaster"
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/clone_lib="RPCI-98"
/clone="BRCR14899"
/clone="end: TET3"
/note="end: TET3"
80 c 204 g 179 t 308
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hes 53;
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1091 WDRDTRKDDWDWTKWWTWWKDRADDRRWAGDADRWAWDDGAGTWWTATWWWWWWWATWD 1032
                                  1004 aactttctgaagtggtcctcaaaagaaatgaagatgaaaatggaaaatggaaaactgaagagactc 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02 JUN-199) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Collaboration with the Berkeley Drosophila Genome Project (BDGP).
- Collaboration with the Berkeley Drosophila Genome Project (BDGP).
- The BDGP is constructing a physical map of the Drosophila
- The BDGP is constructing a physical map of the Drosophila
- In the BDGP prosophila please see http://www.fruitfly.org The BDGP Drosophila
- In the BDGP Drosophila
- In the BDGP Drosophila
- In the BDGP Drosophila
- Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
- Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
- NY. The library is named RPCI-98 and was constructed by partial
- NY. The library is named RPCI-98 and was constructed by partial
- NY. The library is named RPCI-98 and was constructed by partial
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- NY. The library is named RPCI-98 and was constructed by partial
- NY. The library is named RPCI-98. The Same strain used for the BDGP's
- isogenic strain y2; cn bw sp, the same strain used for the BDGP's
- isogenic strain y2; cn bw sp, the same strain used for the BDGP's
- isogenic strain y2; cn bw sp, the same strain used for the BDGP's
- isogenic strain y2; cn bw sp, the same strain used for the BDGP's
- isogenic strain y2; cn bw sp, the same strain used for the BDGP's
- isogenic strain y2; cn bw sp, the same strain used for the BDGP's
- isogenic strain y2; cn bw sp, the same strain used for the BDGP's
- isogenic strain y2; cn bw sp, the same strain used for the BDGP's

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pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR08K10"
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                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
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64 c 131 g
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        - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tcagaaattataaatgctaaccaggttgaggattctagaagtgacgaagttcatcgtgaa 1422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WWADAAWWTTTDTDDDDKRDRRRKGARRRRTTARAAWDWWTWKAWDWAKWDWKTRAD
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Pterygota;
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zrygota; Neoptera; Endopterygota; Diptera; Brachycera;
scomorpha; Ephydroidea; Drosophilldae; Drosophila.
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/organism="Drosophila melanogaster"
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                                         Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome sur
BACN16316 of DrosBAC library from
fly), genomic survey sequence.
AL106910
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                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                  Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14D09"
/note="end : TET3"
a 95 c 109 g 2
Location/Qualifiers
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segref@genoscope.cns.fi
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AL065923.1
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AL065973
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part o collaboration with the Berkeley Drosophila Genome Project (BDGP)
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and maron Mammoser in Pieter de Jong's laboratory in the Department
                                                                                                                                                                                                                                                                                                        GSS
                                                                                                                                 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins.
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 884)
                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                          fruit fly.
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/db_xref="taxon:7227"
/clone_lib="DrosBaC"
/clone="BACN16J16"
/note="end: T7"
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Pred. No. 0.012;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 939)
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a Determination with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information melanogaster pancome using these BACs. For further information melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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Drosophila melanogaster genome sur
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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96; Mismatches 248;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

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                     Drosophila melanogaster genome sur
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fly), genomic survey sequence.
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/clone="BACRL2K22"
/note="end : TET3"
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segref@genoscope.cns.fr
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/clone="BACR39G08"
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/db_xref="taxon:7227"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 985)
                                      Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                Eukaryota; Metazoā; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fl
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Web : www.genoscope.cns.fr)
stermination of this BAC-end sequence was carried out as part of
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/clone="BACN37G05"
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
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                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggagattgttgcagtagatcaggagggagctcgtgttgttgggacgaactgtatgcttgc 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTTTNTTTTTTTTTTKTTKTNTGGTTTKKKKKKKKKGTNNTGNNNTGGTKGTTTGNGNTNT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agttgtgcctcggctgtgctggctgtgttgattctctcctcgtcgtggtgatcgatat 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTTTTTKNTTTTTKGGGGGGGGGGTTKKKGGGAARNNNNGGGGGGTNNTTTTNTT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tgcttggattgttgatgtgctaattcgcggcgttacaagatcactgctggattgatattg 182
                                                                                                                                                                                                                                                                                                                                                                                                                                          TTKKGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pBeloBAC11.
                                                                                                                   1 (bases 1 to 706)
Watson, B.S., Shin, H.-S., Lopez-Meyer, M., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., M., G.D. and Palva, N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
               2510
Tel:
                               Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
                                                                         Medicago truncatula nodulated Unpublished (2000) Contact: Paiva NL
                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                              AW684844 706 bp mRNA linear NF022B10NR1F1000 Nodulated root Medicago truncatula
                                                                                                                                                                                                                                                     Medicago truncatula
                                                                                                                                                                                                                                                                                                  AW684844.1
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                                                                                                                                                                                                                                                                                                                              NF022B10NR 5', mRNA sequence.
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Sam Noble Parkway,
580 221 7317
580 221 7380
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN37L10"
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BI176637/c
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AUTHORS
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VERSION
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BI176637
BI176637.1 GI:14642448
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                                                                                                                                                                                                                                                                                                                                                                     potato.
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Similarity 50.9%;
09; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="root"
                                       /clone_lib="cSTE"
                                                     /clone="cSTE5K22"
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997 actccaaaactttctgaagtggtcctcaaaagaaatgaagatgaaaatggaaaaactgaa 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCAAGCCAGAAGATCACCAAGGATGAATATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 022 row: B column: 10 seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                                                                                                                          Generation of ESTs from in vitro grown microtubers Unpublished (2001)
Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 748)
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EST517582 cSTE Solanum tuberosum cDNA clone cSTE5K22
                                                                                                                                                                                                                            For clone info: please contact Research Genetics, pivision tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                             van der Hoeven,R., Bezzerides,J., Bachem,C., Viss
Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: Lambda Zap; Four-week old Rhizobium meliloti-inoculated Medicago truncatula roots, con' a mixture of young and old roots and nodules." a 119 c 175 g 168 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="NF022B10NR"
/clone_lib="Nodulated root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Pooled developmental"
/tissue_type="axillary buds of stem explants;
sink-tubers"
                                                                                                              /organism="Solanum tuberosum"
/cultivar="Bintje"
                                                                                                                                                                                  Location/Qualifiers
                                                                                            /db_xref="taxon:4113"
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Pred. No. 1.2;
0; Mismatches
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BASE COUNT
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Search completed: September 16, 2002, 18:12:16 Job time: 9974 sec
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                                                                                                                                                       337 TGGAATTGTTGCTGTGGCAGCGGCGGGTGCTGGTGCTGGTGCTGCTGCTGCTGCTGC 278
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                                                                                                                                                                                                                                                                                                                                                                                                              208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Wector: pBluescript SK(-); Site_1: EcoRI; Site_2: Anote="Wector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Tissue supplied by Christian Bachem and Richard Visser (Department of Plant Breeding, Wageningen University, The Netherlands). The cSTA libraries will attempt to capture the induction and initiation/initial growth of the tuber in an in vitro system as described in Bachem et al. (Plant Journal, 1996). Small microtubers develop from axillary buds attached to stem explants when placed on a high sucrose medium (10%). Visible morphological changes occur synchronously at day five in the axillary buds. The first library, cSTA (1-20) consists of axillary buds harvested on days 1-3. This targets those genes involved in induction of the microtubers. The following libraries, cSTA (21-40) and cSTA (41-60), capture genes involved in tuber initiation and outgrowth. This library is noted as P3 in Tanksley lab notebooks."
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/lab_host="SOLR"
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Maximum Match 100%
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3: sp_fungl:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe!
9: sp_mage:*
10: sp_plant:*
11: sp_rodent:
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
15: sp_bacteri
16: sp_bacteri
17: sp_archeap
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                                                                                                                                                                                                                                                                                                                                                                                              sp_organelle:*
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sp_unclassified:*
sp_rvirus:*
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Q91w14 oryza sativ
Q947d1 oryza sativ
Q91yd9 arabidopsis
Q9yd6 homo sapien
Q91h98 arabidopsis
Q23587 caenorhabdi
Q44929 drosophila
Q9sz55 arabidopsis
Q22257 caenorhabdi
Q9qj16 human herpe
P91257 caenorhabdi
Q9qj16 caenorhabdi
Q9qj16 drosophila
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Best Local Similarity 100.0%;
Matches 1057; Conservative 0;
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Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza Sattva nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0485D09.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP001859; BAA94774.1; -.
Hypothetical protein.
SEQUENCE 1385 AA; 151678 MW; 16E784264EEFC7B5 CRC64;
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Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Spermatroideae; Oryzeae; Oryza.
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O9LML4;
O1-CCT-2000 (TrEMBLrel. 15, Created)
O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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and flowering in arabidopsis.";
Plant Cell 13:1865-1875(2001).
EMBL; AF326768; AAK98529.1; -.
SEQUENCE 1057 AA; 116447 MW;
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Ehrhartoideae; Oryzeae; Oryza.
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Similarity 99.8%;
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EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ
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Submitted (APR-2000) to t
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Bevan M., Hilbert H.,
Bancroft I., Mewes H.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Arabidophyta; eudicotyle; Core eudicots; Rosid.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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L Local Similarity
ches 250; Conserv
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 ANVSED -- - NTSVDVGALPEVPQITWHIEVNGA -- -
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                                    -ADNAIEEKVGVNCENDDQTATTFLKKARGRPMG----ASNVRSKSRKLVSPEQ---VG
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                                                                                                                                                                                                                                                             189;
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Pred. No. 6.4e-16;
9; Mismatches 403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEEMVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNSQQ--KSLASQSTQKELQGHLALTTQESPH-----PQN---FQSTQEQQTHLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDIPMDIVELLAKNQHERQLM-TETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CP-----PGTQRT--ERKLSLPKKKTKK---PVIDNGKSTVISFSNGIDGSQVNSHTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPMEVSMDIPVSNHTVGEDGLKSSKNKTKRKYSDVVDDGSSLM----NWLNGKK--KRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPFKGKQRNRRFQVVDEFVPSLPCETSQ--EGIKEHDADPSK--RSTPAHSLFTGNDSVP
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                                DRFVRQD-----
                                                                  RKDT----FAPVYNTHEKPVFASSNDQAKFQLLGASNS-
                                                                                                                                                                                                                                                                       NENTWNLNFVAANGKQKCGPNPEFSFGCKHAAGVSSSSRPIDNFSSESSIPALHLLSLL
                                                                                                                                                                                                                                                                                                                                                QYR-----EASHPIWPSS------MIPPQSQYKPVSLNINQSTN-PGTLS--QASN
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                                                                                                                                                                                                                                                                                                                                                                                                                   -----ASSIRFSGHNCQWLGNLPTV--GNQNPSPSSFRVLRA-----CDTCQSVPN
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                                                                                                    HFEALNSGMFSAKWNALQLGSVSSSAD-----FLSARNSTAQSWTRGKGKMVHPL----
                                                                                                                                    SKRFTQEPSRKSFPITPPIGT--SSLSFQNASWSPH------HQEKKTK
                                                                                                                                                                                                          DPRLRSTTPADQHGNTKFTKRHFPPANQSKEFIELQTGDSSKSAYSTK---QIP--FDLY
                                                                                                                                                                                                                                       DPSTLASFP--NYGTS--SRNQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDL
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Best Local Similarity
Matches 210; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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KIAA0624.
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TISSUE-BRAIN;
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                                                                                                                                                                                                                                                      1334 LAPTLOEMASVEAAVSLPEEESKAREIFSDNLAKTPLGDSENKKER------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNNVEDAMGNYMLNKFSPSSPESANECSKVLSDSA---LEAPEATERMTNVKSSGSTSVR 1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGALP-----EVPQITWHIE-----VNGADQPPSTPKLSEVVLKRNEDENGKT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L----IEANQSNSKVSELDTIYCTLPRKSSSFLIHGRQSGSKIMAASLRNGPPPFQI 1048
               MIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDY-----
                                                                                                                                                                                    ---GKKLQSETLHTSLMLQRKNVSEEK-SENCQQSINSSNSGPSSLPA-LSEVNIGNSQT
                                                                                                                                                                                                                                                                           CEDD-----RSTIPVPMEVSMDIPVSNHTVGEDGLKSSKNKTKRKYSDVVDDGSSLMN 452
                                                                                                                                                                                                                                                                                                                         ESPQVETETFPNALEKDKQNYSTREQSGTPSCENLKMSVNSDQTLTTENMTAFRLSNRGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITFVRSTFVPASVGSQKVS------PSTQSS---QGKNADRSTLPKSVQEG-----
                                                                                 ENSVLSHSAK----VSPAEHDIQIMSDLHE------QSLPKK--KKKQKLEVTREKQT
                                                                                                                                                   EISTORCSSKGKT-----AGLSKGKTHSAASTKYG--GESTRNGQNIHVLSAEDQCQMET 565
                                                                                                                                                                                                                        WLNGKKKRTGSVHHTVAHPAGNLSNKKVTPTASTQHDDENDTENGLDTNMHKTDVCQHVS
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                                                 -NKTLSHSESQVFALTPALHKLQLGEETQSDEPNLESLQSEPRELPQRSQEANMTESRK-
                                                                                                                    RRSSWECTGSGRAIPFTGSGKCPQKDHTSTAVGDGSSGSQPREGRG----DIGTNCQKMT
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Pred. No. 6.2e-05;
1; Mismatches 423
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	 SST 892	34 VOSVEAKEKNENGGYDYNVGNKEDSKDIKDDRSVEVKANKEESMKKKREEVORNDK-	3 1	
	PST 253	207 LQGPAQNYDVAANVSEDNTSVDVGALPEVPQITWHIEVNGADQP	QΨ	
	SKD 833	777 GNKKESEKVEKGEKKESKDAKSVETKDNKKLSSTENRDEAKERSGEDNKEDKEE:	ф	
	PMKD 206	SQKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANTDS	Оу	
26	Gaps	uery Match 3.9%; Score 216; DB 10; Length 2081; est Local Similarity 18.9%; Pred. No. 0.00013; atches 155; Conservative 139; Mismatches 382; Indels 144;	Qu Be	
		EMBL; APUU2U5/; BABU31/4.1; SEQUENCE 2081 AA; 232851 MW; D3603E1F85EFFF29 CRC64;	SQ	
		nd BAC ciones."; es. 7:217-221(2000).	P P	
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	:.	Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabaca S Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.	R R	
			R P	
		NCBL_Tax1D=3/02;	RN	
	vostuae,	gnoliopnyta; eudicotyledons; core eudicots; sicales; Brassicaceae; Arabidopsis.	888	
	ta;	ridiplantae; Streptophyta; Embryophyta; Tracheop	80	
		CHROMOSOME 3, BAC CLONE: T19N8.	DE C	
		01-OCT-2000 (TIEMBLIEL, 13, CLEACED) 01-OCT-2000 (TEMBLIEL, 15, Last sequence update) 01-DEC-2001 (TEMBLIEL, 19, Last annotation update)	3 5 5	
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		PRET TWINARY	RESI Q9L	
) - F	Db	
		990 WNALQLGSVSSSADELSARNSIAQSWTRGKGKMVHPLDRFVRQDICITNKNP 1041	Qγ	
	3KE: 1886	DYG	рb	
	SAK 989	LQKEIANWSENCGTQSGYKL	Qy	
	RSF 1846	1795 NVHGDLLRKSHPPKVRERHFSESTSIDNALSRLTLGNEFSVNNGYSRRFRS	В	
	RPL 929	KGSTSTSYG	Qy	
	KŠI 1794	1755 -AQKSRVSSPLASFLQQQRSASSLEWEPEPHLYRSKSLKS	DЬ	
	ASF 869	.RAVNQVHARNFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHILRMMI	Qy	
	EP 1754	1711 KDVTAAQNLVRESGAPSPITETSLREAEFSDNQRRLSPPE-PL	Dβ	
	LDR 809	750 KDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIAPLDR	Qy	
	ENS 1710	ITVLPNREPSTHVSNQKSNSISQRHQNEFKNVSESPSKH	DЬ	
	vGR 749	WEEWTIAASSPLFSHHDDQYIAEAPT	Qy	
	IGE 1650		Db	
	708	-QSTC	Оy	
	RLA 1590	1549AEDEMQKSAWDQPSLPEGNKNKTNLDDLVKGENRSSVKHRLA	Db	

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Q23587;
01-NOV-1996 (TrEMBLTel. (
01-NOV-1996 (TrEMBLTel. (
01-DEC-2001 (TrEMBLTel. 1
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
MISON R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulso
Bonfield J., Burton J., Connell M., Favello A., Fulton L.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M
                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
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STRAIN-BRISTOL N2;
Favello A., Vaudin M.;
The sequence of C. elegans
The sequence of C. the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shown Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaudyan K., Waterston R Watson A., Weinstock L., Wilkinson-Sproat J., Wholdman P., "2.2 Mb of contiguous nucleotide sequence from chromosome III elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00010; ASX_HYDROXYL; 9.
PROSITE; PS00102; EGF_1; UNKNOWN_1.
PROSITE; PS01186; EGF_2; 22.
PROSITE; PS01187; EGF_CA; 13.
PROSITE; PS0135; TRYSIN_SER; UNKNOWN_1.
Calcium-bhdding; EGF-114c domain; Glycoprotein; Hydroxylation; SEQUENCE 3507 AA; 365315 MW; 154F0B687874D9DF CRC64;
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                                                  SSEAPVTSTSPTEVHTSSETKPSLSASSTTGDTNSTTPSTSSLASVKSTSAPEGTSASVA
                                                                                                                                                                        P--STQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANTDSPMKDLQGPAQNYDV
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PVKLSSLSPDVSQPSTKTFDATESSTVQASETSSGTSVKSTSEPESHVTKLSITSSNPSS
                         PVSGQKCEQICNEP-----CEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDA
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IPR001881;
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IPR001507;
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EGF_like; 16.
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EMBL/GenBank/DDBJ
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044929;
01.JUN-1998 (TrEMBLrel. 06, Created)
01.JUN-1998 (TrEMBLrel. 06, Last sequence update)
01.JUN-2001 (TrEMBLrel. 17, Last annotation updat)
MICROTUBULE BINDING PROTEIN D-CLIP-190.
CLIP-190 OR CG5020.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSLMNWLNGKKKRTGS---VHHTVAHPAGNLSNKKVTPTASTQHDD--ENDTENGLDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPSQEPAGILTSTVVVPTSSVSLITASEIEAITSNTPFKQGRTPITTSPKSLVKSTTSPS
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                                                                                                                                                                                                                                          TVTCHSLATCEQ----STGVCICRDGFIGDGTTACSKKSTADCISLPSLCADKAKCDNST
                                                                                                                                                                                                                                                                                                PATTSGKRGPPSIQPPAEMFTTPAPPPPSNGGYGEETNQEEEQVTSTTTTEAP---SLCS
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                                                                                                                                                                                                              R-----GKGKMV--HPLDRFVRQDIC 1035
                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                               -----AH-NQYKGSTSTSYGSNLNGKIPLTFEDLSRHQ------
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                                                                                                                    PRT;
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           Hexapoda;
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           Insecta;
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Best Local 9
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Lantz V.A., Miller K.G.;
J. Cell Biol. 0:0-0(1998).
EMBL; AF041382; AAB96783.1; -.
EMBL; AF0401382; AAB96783.1; -.
E1yBase; FB900020503; CLIP-190.
Interpro; IPR000938; CAP-G1y.
Pfam; PF01302; CAP-GLY; 2.
SEQUENCE 1690 AA; 189103 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 LPKSVQE-----GNDSKCNAPSGKNGAAEANTDSPM---KDLQGPAQNYDVAA 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QCNLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKCEQIC-----NEPCEEVVLK 329
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                                                                                                                                                                                         MYTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGI 780
                                                                                                                                                                                                                                         QKSLASQSTQKELQGHLALTTQESPHPQNFQ------STQEQQTHLRMEE
                                                                                                                                                                                                                                                                                      EQELQQLQSKSAESESALKVVQV-QLEQLQQQAAA-----SGEEGSKTVAKLHDEISQ
                                                                                                                                                                                                                                                                                                                                                  EVHLQEIKAQNTQKDLELVESGESLKKLQQQLEEKTLGHEKLQAALEELKKEKETIIKEK 813
                                                                                                                                                                                                                                                                                                                                                                    SVLSHSAKVSPAEHDIQIM------SDLHEQSLPKKKKKQKL-EVTREKQTMIDDI 616
                                                                                                                                                                                                                                                                                                                                                                                                               KQISDLKQLAEQEK-----LVREKTENAINQIQLEKESIEQQLALKQNELEDFQKKQSES
                                                                                                                            QAVDLTSTHVMGSSSNYASRQPVIAPLDRYAERAVNQVHA----RNFPSTIATMEASKL
                                                                                                                                                                                                                         LKSQA-EETQSELK-----STESNLEAKSKQLEAANGSLEEEAKKSGQLQEQITKLKSEV
                                                                                                                                                                                                                                                                                                                    PMDIVELLAKNOHEROLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTNSQ
GSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVGVLGSLLQKEIA-----NWS 950
                                                           CDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYGTSSRNQMESQLHNSQYAHNQYK 895
                                                                                           -----KVNKEYAESRAEASDLQDKVKEITDTLHAELQAERSSSSALHT-KLSKF
                               SDEIATGHKELTSKADAWSQEMLQK------EKELQELRQOLQDSQDSQTKLK 1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.9%; Score 215; DB 5; Length 1690; milarity 19.1%; Pred. No. 0.00012; Conservative 139; Mismatches 352; Indels 234;
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                                                                                                                                                                  ----VESKTKQLEAANAALE----
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PRELIMINARY; PRT; 852 AA.
Q9SZ55;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 92.0 KDA PROTEIN.
F11C18.80 OR AT4G31880.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck

Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck

De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.

Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bevan M., Terryn N., Ardiles W., Buysshaert C., Da
De Clerck R., De Keyser A., Neyt P., Rouze P., Val
Villaroel R., Gielen J., Van Montagu M., Hoheisel
Mayer K.F.X., Schueller C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ data
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EMBL; AL161579; CAB7
Hypothetical protein
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Submitted (MAR-2000) to the EM
EMBL; AL049607; CAB40758 l; --
EMBL; AL161579; CAB79906.1; --
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Pred. No. 0.0001;
7; Mismatches 282;
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Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                  "Genome sequence of the nematode investigating biology."; Science 282:2012-2018(1998). EMBL; 270756; CAA94789.1; -. SEQUENCE 1295 AA; 147395 MW;
                                                                                                                                                                         none;
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                             SSSNYASRQPVIAPLDRYAERAVNQVHARNFPSTIATMEASKLCDRRNAGQVVLYPKESM
                       SWTRGKGKMVHPLDRFVRQDICITNKNPA-----DFTT--ISNDNEY
                                                 QRREEELIAQVSKHRDQQEQLQLTLDELKSAQHSTETSRSQSNELAARIEELEASISFAQ
                                                                                                    ----MNKEMVDELN------AKLGDALE-----GME---ELKKSLEVSEAKV
                                                                                                                           TFEDLSRHQLHDLHRPLRPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQM
                                                                                                                                                       NSSH - - - KRDMVALAS
KALQDVEDVKH----
                                                                                                                                                                                                         ----EEIKQLQLDLQNFKQNAEVLESL---
                                                                                                                                                        ------QLEELQHKLVVGESQVENVKEELIGAKI-----
  -QQDIQISEANEAMVKLKQDFETERTSLQNEF
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Best Local Similarity 18.6%;
Matches 200; Conservative 1
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090J16;
01-MAY-2000
01-MAY-2000
01-DEC-2001
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Viruses; dsDNA viruses, no RNA s
Betaherpesvirinae; Roseolovirus.
NCBI_TaxID=32604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Human herpesvirus 6B genome sequence:
with human herpesvirus 6A.";
virol. 73:8040-8052(1999).
EMBL; AF157706; AAD49674.1;
SEQUENCE 1520 AA; 171362 MW; 0F498E
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Dominguez G., Dambaugh T.R., Stamey F.R., Dewhurst S.,
Pellett P.E.;
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                                                                                                                                                                                                                                                                                                                          SGOKCEQICNEPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDAKLCRRKPKK 370
                                                                                                                                                                                                                                                                                                                                                     NFAVHKTKIHSDSELHHTKKNIHRSKTSL--QDRVLISKHAPRAPTKDNSYKKHHDPKDT
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                                                                                                                                                                                                                            SSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGN-LSNK-----KVTPT 483
                                                                                                                                                                                                                                                     ----SD--PSHNLHGKTSDEQYKTS-----PDNEKISTPPKSKTHHCIHDSSSSEEGQY 559
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                                                                                                  STMNRNCASKKHSAGANKNLTDNSPIRSHSNPSSFTAFNKSNSGNSTMNS----TSNGD
                                                                                                                  EISTQRCSSKGKTAGLSKG------KTHS-----AASTKYGGESTRNGONIHYLSAED
                                                                                                                                                    SKTNHKTEESTENTDLNSFSNENTNKTEIEDSNIIQPFSQLFCNETIIPSTSACPTQETP
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                                                                        QCQMETENSVLSHSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMIDDIPMD
RASSRASSRASSRASSRTSSRASSRAFSRASSRVSSRASSRASSRASSRASSRASS
                        IVELLAKNQHERQLMTETDCSDINRIQSK--TTADDDCVIVAAKDGSDYASSVEDINSQQ
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                                                    -CSSTENKSETSNOTNGENSDKPLSKTFTEVSDRASSRASSRASS
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Last sequence update)
Last annotation update)
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pred. No. 0.00029;
70; Mismatches 480;
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      "Direct Submission.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; UB0022; AAC25885.2; -.
R InterPro; IPR001064; Crystallin.
R InterPro; IPR003961; FNIII repeat.
R InterPro; IPR003961; FNIII.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003598; Ig.c2.
R InterPro; IPR003598; Ig.c2.
R InterPro; IPR003598; Ig.c3.
R InterPro; IPR003006; Ig.MHC.
R InterPro; IPR003006; Ig.MHC.
R InterPro; IPR00130; Zn.MTpeptdse.
R Pfam; PP00041; fn3; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY 1997 (TrEMBLrel. 03, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 385.7 KDA PROTEIN.
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Fulton B., Wohldmann P.;
"The sequence of C. elegi
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613;
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                    Waterston
                                                                                                                                                             STRAIN-BRISTOL N2;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P91257
                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                          None;
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EMBL/GenBank/DDBJ
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Query Match
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Matches 214
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SMART; SM00409; IG; 12.

SMART; SM00409; IG; 12.

SMART; SM00410; IG_11ke; 1.

SMART; SM00410; IG_11ke; 1.

PROSITE; PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN_1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

Hypothetical protein; Immunoglobulin domain; Repeat.

Hypothetical protein; Immunoglobulin domain; Repeat.

SEQUENCE 3484 AA; 385746 MW; 21DD6F6893020F4F CRC64;
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                                                                                                                                                                                                                                                                    KKKIIKKKTEKSDSSISQKSATDSEKVSKQKEQDEPTKPAVSETQMVTEADKSKKQKETD
                                                                                                                                                                                                                                                                                                                                                  VVLK----RSSKSKRKTDKKLMKKQQHSKKRTAQ------ADVSDAKLCRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIKKKETPESEQVTAA---EPEQQKISEVDVQS-VAETEVGAKKKPDAEKPTDLSKAKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214;
RQLMTETDCSDINRIQSKTTADD
                                    GADAVKKQKELDEKNKLEANKKSAAGKLKIEEESAAKSKQTVEEQAKLD~AQTKAKTA-E
                                                                           HEQSLPKKK - - - KKQKLEVTRE-
                                                                                                                  SADKLKLEEQAQAKKAAEVEAAKKQKEKDEQLKLDTEAASKKAAAEKLELEKQAQIKKAA
                                                                                                                                                       G-----ESTRNGQNIHVLSA-----EDQCQMETENSVLSHSAKVSPAEHDIQIMSDL
                                                                                                                                                                                              EKLKLDAEIAAKTKQEADEKSKLDAQEKIKKVSEDDAARKEKELN-DKLKLESEIATKKA
                                                                                                                                                                                                                                   TENGLDTNM-------HKTDVCOHVSEISTQRCSSKGKTAGLSKGKTHSAASTKYG
                                                                                                                                                                                                                                                                                                  KK------KRTGSVHHTVAHPAGNLSNKK-------VTPTASTQHDDEND
                                                                                                                                                                                                                                                                                                                                                                                           EVSMDIPVSNHTVGEDGLKSSKNK------
                                                                                                                                                                                                                                                                                                                                                                                                                                 DEQLKLETEVVSKKSAAEKLELEKQAQIKKAAEADAVKKQKELNEKNKLEAAKKSAADKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKKVRLLSEIINANQVED------SRSDEVHRE----NAADPCEDDRSTIPVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAQKIAEVNKAKKQKEVDDNLKREAEVAAKKIADEKLKIEAEANIKKTNEVEAAKKQKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLEKAADTTKQIETETVVDD----KSKKKVLKKKTEKSDSFISQKSETPPVVEPTKPAES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKCEQICN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVPKKKTIKKKTEKSD----SSISQKSNVLKPADDDKSKSDDVTDKSKKTTEDQTKVATDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVP-QITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKT-----EETLVAEQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVEDKKDASQPSSSKESSPPTDGKKKKQIPKALFIPDEISSRFGDPSTMHSETNITTTIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- QKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKTSDNGTAPRTLPAKQNGT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 206; DB 5; Le
Pred. No. 0.0011;
1; Mismatches 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -QGPA-QNYDVAANVSE----DNTSVDVGALP
                                                                           KOTMIDDIPMDIVELLAKNOHE
                                                                                                                                                                                                                                                                                                                                                                                             -TKRKYSDVVDDGSSLMNWLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3484;
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  -DCVIVAAKDGSD
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Matches 175
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                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Sun H., Geisel C.;
"The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 231.2 KDA PROTEIN.
                                                                     SMART; SM00060; FN3; 3.
SMART; SM00409; IG; 3.
Hypothetical protein; Re
SEQUENCE 2083 AA; 231
                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         751
                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                900
                                                                                                                                          "Direct Submission.";
submitted (AUG-2001) to the EMBL/GenBank/DDBJ
EMBL; AC024760; AAR59460.2; -
InterPro; IPR003962; FNIII_repeat.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                     Submitted
                                                                                                           InterPro; IPR003599; Ig. pfam; PF00041; fn3; 2. PRINTS; PR00014; FNTYPEIII
                                                                                                                                                                                             Waterston R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLKLDTEAASKKAAAEKLELEKOSHIKKAAEVD-AVKKOKELEEKORLESEAATK---KA 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETOKVADAARKOKETDEKOKLEAEITAKKSADEKSKLEAESKLKKAAEVEAAKKOKEKDE 1305
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175; Conser
 MEIVAVDQEGARVVGTNCMLARGGTGAVAPVLELTATP--
                                                                                                                                                                                                                                    ence of C. elegans (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                       Conservative
                                  3.7%;
                                                                          Repeat.
231174 MW;
                          135;
                                                                                                                                                                                                                                      cosmid Y38B5A.";
EMBL/GenBank/DDBJ databases.
                        Score 205.5; DB 5;
pred. No. 0.0006;
5; Mismatches 435;
                                                                           9270303ADE2D7C2F
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                             Indels
                                              Length
                                                                             CRC64;
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RESULT 13
076891
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GN FUTSCH
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 O76891;
01-NOV-1998 (TrEMBLrel. 08, Careated)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
EG:49E4.1 PROTEIN.
FUTSCH OR EG:49E4.1 OR CG3064.
                                                                                                                                                                                                    1275
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IELVPNEEYAFRIVAVNGF----GEGAPSEIIEVNTLDYDQEESEDFAGEEELKLDDVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSVAKERRWDCSKCLDKLKTSDNGTAPRTLPAKONGTSDGCSITFVRSTFVPASVGSOKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNPSDESAKKDVNEDTAVSSIVKKDDKDVN----KKSLPESGL-TTKKEIQGKPEKKIMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEVS-----SDITSSLEITTESTIPDTAPESQETLNVEIAVT---ETTV-----OKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANVSEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETLVA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANTDSPMKDLQGPAQNYDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKTEKADSSISETS----ETLIKDLTQTKQSEPEPAKRTTETSVQ--DEVKRKTETTSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AADPCEDDRSTIPVPMEVSMDIPVSNHT------VGEDGLKSSKNKT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQ---TTEEHPQPGGKSDSSISSTSDASEVKQVQQSESEAQKVTEKPETAKLESKSKMTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQCNLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKCE-QICNEPCEEVVLKRSSKSKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSHSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMID-----DIPMDIVEL 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKSDTSKTVAESAGSSESETOKVADATSKOKETDKKOKLEAETTAKKSADEKSKLETESK 1070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAK-----DGSDYASSVFDTNSQQK 678
                                                                                                                                                                                                    ---PSESETQKVADAARKQKETDEKQKLEAEITAKKSADEKS
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                                                                                                                                                                                                                                                                                                                                            KLEEESAAKSKQ---TVEEQAKLDAQTKEKTAEKQTGLEKDDKST---
                                                                                                                                                                                                                                                                                                                                                                           SLASOSTOKELOGHLALTTQESPHPONFOSTOEOQTHLRMEEMVTIAASSPLFSHHDDQY 738
                                                                                                              PRELIMINARY;
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Best Local S
Matches 225
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase;
SEQUENCE
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Papagiannakis G., Spanos
"Sequencing the distal X
Submitted (JUL-1998) to t
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INR - - - IQSKTTAD-
                                                                                                                                                                                       TPSAPEHISRADSPAECASEEIASQDKSPQVLKESSRPAWVAESKDDAAQLKSSVEDLRS
                                                                                                                                                                                                                                                              KLQTDSSPVDVAEGDFSHAVA-----SVSTVTPTLTKPAELAQIGAAKTVSSPLDEALR
                                                                                                                                                                                                                                                                                                                                                                                                             LDKPQIIK-----DDKSTEHSRRESL----EDKSAVTSEKSVSRPLSVASDHE
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                                      DVAHASVQPAELSKVDIEKTASSPIDEAPKSLIGSPAEERPESPAESAKDAAESVEKSKD
                                                                                                                                                GQNIHVLSAE----DQCQMETENSVLSHS----AKVSPAEH-----DIQIMSDLHEQSLP-
                                                                                                                                                                                                                                                                                                 KKK-----RTGSVHHTVAHPAGNLSNKKVTPTAS----TQHDDENDTENGLDTNMH
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5327 AA; !
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chromosome of Drosophila melanogaster.";
the EMBL/GenBank/DDBJ databases.
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Pred. No. 0.00
74; Mismatches
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             RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barlow R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davaroport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Days A.D., Dew I., Dietz S.M.,
RA Durbon K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbon K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Lasko P., L., Liu X., Mattei B., Mc.
Liu X., Mattei B., Mc.
Morkulov G., Milshina
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Pterygota; Ne
Ephydroidea;
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
a; Drosophilidae; Drosophila.
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RDR Gience 287:2185-2195(2000).
DR EMBL; AE003750; AAF56376.1; -
DR EMBL; AE003750; AAF56376.1; -
DR FlyBase; FBgn0039257; CG13648.
DR InterPro; ITR001007; VWFC.
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SMART; SM00214; VWC; 4.
PROSITE; PS01208; VWFC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAKONGTSDGCSITFVRSTFVPASVGSQKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKEEPSEPSTGAPTKDE---PAEPSTDAPES------DESKETPESEVPTTVA 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAEIPOPSTETGIKOODETTAAPSIDRKEPYVTEIDEEATTVAPISEKDEKPTEEEKPVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APSGKNGAAEANTDS-----PMKDLQGPAQ---NYDVAANVSEDNTSVDV------GA 231
                                                                                                                                                                                                                                                                                                                                                                                                                            QKPTGEEPS--EEEEKEKPIEQDVSTEG--PVSTEASEAGSTESSEEV-----KPST
                                                                                                                                                                                                                                                                                                               EVHRENAADP-----CEDDRSTIPVPMEVSM--DIPVSNHTVGEDGLKSSKNKTKR 438
                                                                                                                                                                                                                                                                                                                                                    EGEVAEKPEDKQPSSTAQAPVETIPEISTELPAQDGDKPTSEAPVDSDEDTSAPSDEKIP
                                                                                                                                                                                                                                                                                                                                                                                          DKKLMKKQQHSK-KRTAQADVS-----DAKLCRR----KPKKVRLLSEIINANQVEDSRSD 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                               QCNLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKCEQICNEPCEEVVLKRSSKSKRKT 338
                                                                                                                                                    ----DENDTENGLDTNMHKTDVCQHVSEISTQRCSSKGKTAG-LSKGKTHSAASTKYGG
                                                                                                                                                                                                    SVTQVSDVATSTSAPVAG----GDIEKDEQATTASPE---EEEEIKPTIAPAAEIPQPS
                                                                                                                                                                                                                                       KYSDVVDDGSSLMNWLNGKKKRTGSVHH----TVAHPAGNLSNKKVTPTASTQHD----
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KKKKKQKLEVTREKQTMIDDIFMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDC 655
                                                                                                                              EKEPVDEQEVESGTKATPAESD
                                                                                       ESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAEHDIQI------MSDLHEQSLP
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                                                           ----EESTTVASA-ASPAVHDDEIKDVTTTQPVADEKEVAAP
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Pred. No. 0.0011;
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                                                                                                                                    ----ATSGPIDEAST--AAPTK---
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RX MEDLINE-20196006; PubMed=10731131;
RA Adams M.D., Celniker S.E., Hollt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Hollt R.A., Evans C.A., Galle R.F., Almanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Honderson S.N., RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Honderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Honderson S.N., RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Bardon R.C., Mays A. D., Bayraktaroglu L., Beasley E.M., RA Burlis R.G., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M., Paka Borkova D., Botchan M.R., Bouck J., Broktein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Broktein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Broketain P., Bhandari I., Beasley E.M., Deborkova D., Botchan M.R., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P., RA Goldek A., Gong F., Gorrell J.H., Gu Z., Glabar W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glan P., Harris M., Glasser K., RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Harvey D., Helman T.J., Hernandez J.R., Houck J., Lai Z., Liang Y., Lin X., RA Hostin D., Houston K.A., Nobarry C., Morris J., McShrefi A., RA Merkulov G., Mishina N.V., Mobarry C., Morris J., McShrefi A., RA Halsko P., Kelson K.A., Nison K., Nusskern D.R., Pacleb J.M., Ra Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X., RA Halsko P., Kelson K.A., Nison K., Sungkern D.R., Pacleb J.M., Ra Shlee B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shen H., Shen B.C., Stokeler F., Shen H., Ra Flering S., Yao Q.A., Weinstock G.M., Weinstock G.M., Weinsenbach J., Wang S., Yao
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01-MAY-2000 (TrE
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CG3950 PROTEIN.
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Last annotation updat
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EMBL; AE003438; AAF46171.1; -.
F1yBase; FBgn0029975; CG3950.
SEQUENCE 2951 AA; 332269 MW; 85CCCOABBDAC8A2B
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HNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVGV----LGS | | : | | | : : : | | : : : :
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                                                                                                                                   DSTTPIAPGKTSPHG--KPPVKPRERSASPAQKR---RISPPGKQSPGDRSTTTTTKVTT
                                                                                                                                                                                                                                                     IAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAV
                                                                                             LCDRRNAGQVVLYPKESMPA-----THLLR--MMDPSTLASFPNYGTSSRNQMESQL
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-DEDDSSPPLLDAR--VVREFKKVESQQSLPEDARYVRR 2778
                   LGSVSSSADFLSARNSIAQSWTRGKGKMVHPLD-RFVRQ
                                                                    LKKKATPPAEEPCETKQEVTGYVIEEQFYSDNKSPPRHERKELIYSSNADELAAIKQQLQ
                                                                                                                                        --GKITRTMTSSSTTTSSSSSTTNTRNKQREEDSITSSY-----GVGFTDENGLPLFGIRA
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Search completed: September 16, 2002, 22:34:15 Job time: 654 sec

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(without alignments)
1783.728 Million cell updates/sec
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Peptide #2376 enco
Peptide #2403 enco
Protein #2313 enco
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                                    Human brain expres
Human bone marrow
Peptide #2327 enco
cerevisiae apopt
elegans UNC-53
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Human polypeptide	AAM39097	22	2663	3.3	184.5	45
Drosophila melanog	ABB67502	22	3257	3.4	187	44
3	AAR81505	17	1863	3.4	187	43
	ABB59948	22	1489	3.4	187	42
	ABB63410	22	1420	ω. 4	187	41
	ABB66878	22	2586	3.4	187.5	40
	AAM4 0002	22	2505		188	39
Drosophila melanog	ABB58514	22	2897		188.5	38
Novel human diagno	ABG06505	22	2633	٠	191.5	37
Murine Natural Kil	AAR13320	12	982		191.5	36
Drosophila melanog	ABB62899	22	3201		192	35
Staphylococcus aur	AAU37018	22	3158		192.5	34
Staphylococcus aur	AAU34207	22	2025		192.5	33
Drosophila melanog	ABB65391	22	1803	٠	193.5	32
Human carbastatin	AAR05701	11	673	٠	194.5	31
℧	ABB68370	22	1730		195	30
Novel human diagno	ABG16636	22.	2519	3.6	196.5	29
Human protein SEQ	AAM80269	22	2515		196.5	28
Human protein SEQ	AAM80268	22	2515		196.5	27
Human secreted pro	ABB12281	22	2515	•	196.5	26
Human calpastatin.	AAR85596	17	694	•	197	25
	AAY70008	21	754	٠	197.5	24
	AAY85577	21	1552		198	23
	ABB61173	22	1690		198.5	22
	ABB61144	22	1690		198.5	21
Drosophila melanog	ABB60327	22	3111		200	20
0	AAU37120	22	2344		201	19
	42	22	1784	٠	201.5	18
Plasmodium falcipa		21	665		201.5	17
Ď,		10	647		201.5	16
	029	22	2951		204	15
Drosophila melanog	ABB68397	22	2768	٠	204	14
	37	22	2070		206.5	13
C. elegans UNC-53	AAW20057	18	1583	٠	208	12

ALIGNMENTS

RESULT AAY84833

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AAY84833 standard; Protein; 1096 AA

08-AUG-2000 AAY84833;

(first entry)

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An isolated nucleic acid molecule comprising embryonic flower genes is useful for modulating reproductive development in plants
                                                                                                          09-OCT-1998;
                                                                                                                                                                                                   Embryonic flower gene-1; EMF-1; reproductive development; flowering; early flowering; uniform flowering.
                                          WPI; 2000-317987/27.
N-PSDB; AAA14873.
                                                                      Sung ZR, Aubert D,
                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                                           08-OCT-1999;
                                                                                                                                                               WO200022132-A2.
                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                              Amino acid sequence of the EMF-1 gene
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                                                                                                          98US-0169696.
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Claim 7; Page 34-38; 38pp; English.

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                                nntsrppkpcssnarree---hfpmgrqqnshdffpisqpyvpspfgifpptqenr----
                                                                   TNSQQ--KSLASQSTQKELQGHLALTTQESPH------
                                                                                                  DDIPMDIVELLAKNQHERQLM-TETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFD
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                                                                                                                                                                                                           HSAKVSPAEHDIQIMSDL--
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         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, diagnostics, forensics, gene mapping, identification or responsible for genetic disorders or other traits and
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{\tt amskasrkfpakdvsprrhvatifpqsgsrsgfdhlslgtvecnplfpeptpksaesige}
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                                                          ----ASSVEDTN--SQQKSLAS---QSTQKELQGHLALTTQE-----SPHPQNFQS---
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Pred. No. 1.5e-07;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
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23-AUG-2000; 2000US-0649167
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food supplement; medical imaging; diagnostic; genetic disorder.
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene
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26-MAY-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                            HHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRN--SPAATCGA--QFRP-----GIQAV
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No. 9.7e-08;
Lsmatches 311;
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Best Local :
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                               measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exoruncelic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting,
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                                                                                                                                                                                                                                                                                                    from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                               173
 692
                                                                                                                                                                                                                        Local Similarity
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eptenrertanekttpfpaeptenrertane-nttpspagptengdrtplanekttpsla
                                                                                                                              TLPKSVQEGNDSKCNAPSGKNGAAEANTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGAL
                                                                                                                                                      drtplanekttpslaeptengg-----rtpfanekttsssaepteheertplanen
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                                                tenrertanekttsspaeptenggrtpfanekttsspaeptehgertplane-nttlspa
                                                                           PEVPQITWHIEVNGADQPPS----TPKLSEVVLKRNEDENGKTEETLVAEQCNLTKDP-
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zing gene expression in
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234587.
2000US-0236359.
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19.4%;
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Pred. No. 9.7e-08;
5; Mismatches 311;
                        RDQVAEQCNLTKDP-----KPVSGQKCEQICN
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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cardiovascular disease;
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(MQLE-) MOLECULAR DYNAMICS
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                                   04-OCT
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2000US-0632366.
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                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                         hypertension;
                                                                                                                                                                                                                                                        heart; microarray; vascular system;
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measuring human gene expression in a sample derived from human heart (se ABA21535-ABA41305). The present sequence is a protein encoded by one suc probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                Claim 15;
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                                                                                                                                                                                                                                                                                                           2001-488899/53.
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Sequence

1325 AA;

Š Ωy B δÃ B Qy В δõ Дb Qy 망 Qy В δõ 멍 Ωy Вþ Ωy 밁 Query Match Best Local Sin Matches 153; 1060 1004 633 587 536 625 576 944 886 480 841 425 786 381 321 692 287 233 751 TLPKSVQEGNDSKCNAPSGKNGAAEANTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGAL drtplanekttpslaeptengg-----rtpfanekttsssaepteheertplanen DKLKTSDNGTAPRTLPAKQNGTSDGCSITFVRSTFVPASVGSQKVSPSTQSSQGKNADRS 172 PEVPQITWHIEVNGADQPPS----TPKLSEVVLKRNEDENGKTEETLVAEQCNLTKDPttp-spaeptenr----ertanenttpsp----agptenremtan---ekttlfpaep GKTHSAASTKYGG---nttsspaeptenrertanekttqfpaeptenrestanekttpfpae----ptenrewta EPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDAKLCRRKPKKVRLLSEIINA 380 eptenrertanekttpfpaeptenrertane-nttpspaqptengdrtplanekttpsla NPMSGKE-----AKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTN--ektipspakptehe-emtpsanenttpspvkptehgekttlanekitlspegp------VSPAEHDIQIMSDLHEQSLPKKKKK---dttpssaeptengertplanentttsptestehgertanekttpspaeptehgertpsan ttpssaeptehgertplanei-ttpsraeptehgerianekatpspakptehgett-vne VTPTAS---TQHDDENDTENGLDTNMHKTDVCQHVSEISTQRC-----SSKGKTAGLSK nenttlspaepteh----GEDGLKSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGN-----LSNKK NQVEDSRSDEVHRENA - - - epteng--krtpfanekttsssaeptehaer--tenrertanekttsspaeptenggrtpfanekttsspaeptehgertplane-nttlspa Similarity Conservative 4.0%; eemtplan----ekttls----paeptengertpftnek 125; ---ADPCEDDRS----TIPVPMEVSMDIPVSNH--TV Score 220; DB 22; Pred. No. 9.7e-08; 5; Mismatches 311; ----ESTRNGQNIHVLSAEDQCQMETENSVLSHSAK RDQVAEQCNLTKDP-----KPVSGQKCEQICN -QKLEVTREKQTMIDDIPMDIVELL Length 1325; -----tplane Indels 198; Gaps 1059 1003 479 424 785 750 320 691 232 586 943 885 286 674 38;

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                                                                                                                   Query Match
Best Local
                                                                                                Matches 153;
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure genomic suppression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by one of the present sequence is a protein encoded by the present sequence is a protein encoded by the present sequence is a protein encoded by the present sequence is a protein encoded by the present sequence is a protein encoded by the present sequence is a protein encoded by the present encoded by the present encoded by the present encoded by the present encoded by t
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brains -
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drtplanekttpslaeptengg-----
                                                                                                                   Similarity
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                              Conservative 125;
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Pred. No. 9.7e-08;
5; Mismatches 311
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RESULT
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                                                                                                    microarray;
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                                                                                                                     bone
                                                                                                                                                                                                                                      standard;
                                                                                                     cancer;
                                                                                                                   marrow expressed exon; gene
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                      Protein; 1325
                                                                                                     leukaemia; lymphoma; myeloma
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                                                                                                                                                  encoded
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                                                                                                                     analysis;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone {\tt marrow} -
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                                                                                                                                                                             GEDGLKSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGN-----LSNKK 479
                                                                                                                                                                                                                   nttsspaeptenrertanekttqfpaeptenrestanekttpfpae----ptenrewta 840
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                                          dttpssaeptengertplanentttsptestehgertanekttpspaeptehgertpsan
                                                                                                                                VTPTAS--TQHDDENDTENGLDTNMHKTDVCQHVSEISTQRC-----SSKGKTAGLSK 530
                                                                                                                                                            nenttlspaepteh-----eemtplan----ekttls----paeptengertpftnek
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                                                                                                   ttpssaeptehgertplanei-ttpsraeptehgerianekatpspakptehgett-vne
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--VSPAEHDIQIMSDLHEQSLPKKKKK----QKLEVTREKQTMIDDIPMDIVELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1325 AA;
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-02346359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 220; DB 22;
Pred. No. 9.7e-08;
Pred. No. 311;
                                                                                                                                                                                                                                                                                                                                                                    -RDQVAEQCNLTKDP-----KPVSGQKCEQICN
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                                                                        ESTRUGQNIHVLSAEDQCQMETENSVLSHSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1325;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                Probe; human; breast disease; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-2001
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                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #2327 encoded by probe
                                                                                                                                                        Novel single exon nucleic acid probe used to in a human breast .
                                                                                                                                                                                    WPI; 2001-476286/51
                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                  21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                     inflammatory disease;
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                                                                                                                                      Claim 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SQQKSLASQSTQKELQGHLALTTQESPHPQNFQSTQEQQTHLRMEEMVTIAASSPLFS
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                                                                                                                                                                                                     SG,
                                                                                                                                                                                                                      MOLECULAR DYNAMICS INC
                                                                                                                                      SEQ ID No 12385; 322pp; English.
                                                                                                                                                                                                     Hanzel
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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2000US-0236359.
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breast disease;
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences.

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                                            AAG70791;
                                                                AAG70791 standard;
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                                                                                                                                                             kgkntpvpekptenlgn---ttlttetikapvkstenpektaavtktikpsvkvtgdksl 1226
                                                                                                                                                                            HHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRN--SPAATCGA--QFRP-----GIQAV
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 apoptosis associated protein YMR230W.
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Length 1165;

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The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the S. cerevisiae
                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 218pp; English
                                                                                                                                                                                                                                                                                                                                                 Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases .
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Nelissen BJM,
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the invention.
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(BOGA/) BOGAERT T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The UNC-53 protein variants 8A and 7A of Caenorhabditis elegans are new. The UNC-53 proteins and nucleic acids are useful as medicaments to promote neuronal regeneration, revascularisation or wound healing, or for treatment of chronic neurodegenerative diseases (e.g. Alzheimer's or Huntingdon's disease) or acute traumatic injuries. Transgenic cells and organisms transfected with UNC-53 cDNA can be used to determine whether a substance is an inhibitor or enhancer of the regulation of cell shape or mothlity or the direction of cell migration by screening for a phenotypic change in the cell. Inhibitors can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the cDNA sequences can be used to identify homologues of the C. elegans unc-53 gene. The UNC-53 protein can be used to identify proteins which are active in the signal transduction pathway that can be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans UNC-53 protein 8A and 7A variants promote neuronal regeneration, revascularisation or wound
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LDTNMHKTDV--CQHVSEISTQRCSSKGKTAG----LSKGKTHSAASTKYGGESTRNGQN
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19.5%; Pred. No. 1.1e-06;
ative 174; Mismatches 427
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           Bogaert
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         Τ,
                                 BOGAERT T.
STRINGHAM E.
VANDEKERCKHOVE J.
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UNC-53 protein variants 8A and 7A of Caenorhabditis elegans are new. The UNC-53 proteins and nucleic acids are useful as medicaments to promote neuronal regeneration, revascularisation or wound healing, or for treatment of chronic neurodegenerative diseases (e.g. Alzheimer's or Huntingdon's disease) or acute traumatic injuries. Transgenic cells and organisms transfected with UNC-53 CDNA can be used to determine whether a substance is an inhibitor or enhancer of the regulation of cell shape or motility or the direction of cell migration by screening for a phenotypic change in the cell. Inhibitors can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the CDNA sequences can be used to identify homologues of the C. elegans unc-53 gene. The UNC-53 protein can be used to identify proteins which
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans UNC-53 protein 8\mbox{A} and 7\mbox{A} variants -promote neuronal regeneration, revascularisation or wound 1\mbox{A}
Sequence
                                                                    are active in the signal transduction pathway that can be used
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DB; AAT71315.
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Query Match Best Local S Matches 231 383 342 440 291 274 239 224 184 167 128 68 83 14 VGTNCM-----LARGGTGAVAPVLELTATPRODAAAEAGVDEPAQHQCEHFSIRGYVAL Local Similarity 19.5 les 231; Conservative lgldcskltktdidsgnlgavlqllfllstykq pppavpprdt-----qptigvvspimah-----kkltndpvisekpepeklqsms LMKKQQHSKKRTAQADVSDAKLCRRKPKK-----VRLLSEIINANQVEDSRSDEVHRENAA IHVLSAEDQCQMETENSVLSH-SAKVSP----AEHDIQIMSDLHEQSLPKKKKKQKLEV idt----tdvpplpplksvvplkmtsirqpptydvllkqgkitspvks-fgyeqs----- ${\tt sstsdekspssddltlnasivtairqpiaatpvspniinkpveekptlavkgvkstakkd}$ DPCEDDRSTIPVPMEVSMDI------PVSNHTVGED-----GLKSSKNKTKRK iisqq-----dskrcsksseeesgyagfnstsptssstegsls--mhstssk ----sklaapkavstpklasvktigakqepdnsggggggmlklklfssknpssssnspqp TWHIEVNGADQPPSTPKLSEVV----LKRNEDENGKTEETLVAEQCNLTKDP-----NPMS stistsakslessstyssisnlnrptsqlqkpsrpqtqlvrva---tttkigs----tsrlqtpqsriskidsskigikpktsglkppsssttssnntnsfr---pssrssgnnnvg PAK-QNGTSDGCSITFVRSTFVPASVGSQKVSPSTQSSQGKNADRSTLPKSVQEGND---LQKKDPKFCSLSRIFHDQKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKTSDNGTAPRTL LDTNMHKTDV--CQHVSEISTQRCSSKGKTAG----LSKGKTHSAASTKYGGESTRNGQN YSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGNLSNKKVT--PTASTQHDDENDTENG trkaaavpqqqtlskiaapvksglk-----pptsklgsatsmsklctpkvsyrktdap -----klrqlkkdqkkleqlptsimppavsklpsprvatsatasatnpnsnfpqms 166 -SKCNAPSGKNGAAEANTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGALPEVPQI --sasedsivahasaqvtpptktsgnhsl-----3.8%; 3%; Score 208; DB 18; 5%; Pred. No. 1.1e-06; 174; Mismatches 427 Length 1583; errmgknktsessgy Indels 350; Gaps 439 397 341 67 487 427 238 582 532 497 382 290 273 223 183 57;

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                     31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic
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CC diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences for the printed control of the product of the printed control of the product of the printed control of the product of the printed control of the product of the printed control of the product of the printed control of the product of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of the printed control of
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences. Sequence sequences (ABL01840-(ABB57737-ABB72072). 2768 AA WIPO 18

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Conservative 118;

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KKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDC::|:||:|||:|||
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                                                                                                                     ekepvdeqevesgtkatpaesd-gqpideiap----atsgpideast--aaptk---
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                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                     The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic genes from Drosophila
     Sequence
                                                                                                                                          sequences (ABL01840 (ABB57737-ABB72072)
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                                                                                                              --gkitrtmtssstttssssttntrnkqreedsitssy----gvgptdenglplfgira
                                                                                                                                    HNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVGV----LGS : | | : | | : : : :
                                                                                                                                                                                    tsttrga----pskpaggpiwadrskvlkghatvpqtngstprkgstssttsss--
                                                                                                                                                                                                                                                           dsttpiapgktsphg--kppvkprersaspagkr---risppgkqspgdrstttttkvtt
                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSVFDTNSQQK----SLASQSTQKELQGHLALTTQESPHPQNFQSTQEQQTHLRMEEMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        meddspve----prnpnssvkf-----dvprksssrgadeprktslkgkdedsdlele
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                                     lkkkatppaeepcetkqevtgyvieeqfysdnkspprherkeliyssnadelaaikqqlq
                                                                            LLQKEIANWSENCGTQ---SGYKLG---VSTGITSHQMNRKEHFEALNSGMFSAKWNALQ
                                                                                                                                                                                                                          LCDRRNAGQVVLYPKESMPA-----THLLR--MMDPSTLASFPNYGTSSRNQMESQL
                                                                                                                                                                                                                                                                                                                                                                    I AASSPLFSHHDDQY I AEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAV
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     LGSVSSSADFLSARNSIAQSWTRGKGKMVHPLD-RFVRQ
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Search completed: September 16, 2002, 22:23:16 Job time: 8005 sec

OLIGINAMA BELEFA SIHI

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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
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Maximum Match 100%
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                       1371
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LENGTH: 1848 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: UFILING DATE: 25-AUG-1CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 16-AUG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Trecartin, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: United States ZIP: 94111-4187
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PAPENSINTGSATTMTETAEKSDKPQ--METVTENDRQPEANTVADNSVANNSESS----
                                                                                                                                                                                                                                                                                  GNLSNKKYTPTASTQHDDENDTENGLDTNMHKTDVCQHVSEISTQRCSSKGKTAGLSKGK 532
                                                                                                                                                                                                                                                                                                                                                                         PVSNHTVGEDGLKSSKNKTKRKYSDVVDDGSSLM-----NWLNGKKKRTGSVHHTVAHPA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EATQSEGKTEETQTAETKSEPTESVTVSENQPEKTVSQSTEDKVVVEKEEKAKVETEETQ 1204
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                                                                                                         SLPKKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTAD
                                                                                                                                                    AKPQAQAKPQTEPAR - - ENVSTVNTKEP - QSQT
                                                                                                                                                                                              THSAASTKYGGESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAEHDIQIMSDLHEQ 592
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415) 398-3249
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RESULT 3
US-08-425-061-20
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Patent No. 5622829
                                                                                                  TELEFAX: (415) 494-87
TELEX: 910 27729
INFORMATION FOR SEQ ID NO:
                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59
TELECHOMOUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
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APPLICANT: KING, I
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APPLICANT:
APPLICANT:
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
STATE: California
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: GENETIC MARKERS FOR BREAST TITLE OF INVENTION: CANCER
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                                                                                  SEQUENCE CHARACTERISTICS:
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TOPOLOGY: 1
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                              STRANDEDNESS:
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                                                                  ENGTH:
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                                              amino acid
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4 Embarcadero Center, Suite 3400
                                                              900 amino acids
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US-08-425-061-20

δÃ 밁 밁 Š 밁 ρ Š δõ Q 밁 δÃ В QΥ 밁 Qy В Q 밁 Š Qy Š 밁 δõ 밁 Q 밁 Q 밁 B B 밁 δã 맑 Query Match
Best Local Similarity
Matches 200; Conserv 147 844 583 532 482 471 424 421 368 371 324 SKETCND-----RRTPSTEKKVDLNADPLCERKEWNKQKLP-----CSENPRDT 367 315 270 216 157 694 634 276 VAEQCN------LTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQK-----204 104 RRWDCSKCLD-----732 87 31 IKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQE----STRFSQLVEEL 86 48 VVLYPKESMPATHLLRMMDPSTLASFPNYGTSSRNQMESQLHNSQYAHNQYKGSTSTSYG 903 ----VRLLSEIINANQVEDSRSDEVHRENAADPCEDDRSTIPVPMEVSMDI-----PVS LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146 QLMTE---TDCSDINRIQSK-----TTADDDCVIVAAKDGSDYASSVFDTNSQQKSLAS GSSEKIDLLASDPHEALICKSERVHSKSVE--SNIEDKIFGKTYRKKASLPNLSHVTENL 481 NHTVGEDGLKSSKN-----KTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAH-----CEQICNEPCEEVVLKRSSKSKRKTD---KKLMKKQQHSKKRTAQADVSDAKLCRRKPKK-HVEPCGTNTHASSLQHENSSLLLTKD-----RMNVEKAEFCNKSKQPGLARSQHNRWAG VAANVSEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETL 275 VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD 215 ------KLKTSDNGTAPRTLPAKQNGT------SDGCSITFVRSTFVPASVGSQK 156 VDEPAQHQCEHFSIRGYVALL -- OKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103 SHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRN-----SDTFPELK - - - - LTNA - - - - PGSFTKCSNTSELKEFVNPSLPREEKEEKLETVKVSNN - -QSTQKELQGHLALTTQESPHPQNF---QSTQEQQTHL-----RMEEMVTIAASSPLF 731 PNCTELQIDSCSSSEEIKKKKYNQMPVRHSRNLQLMEGKEPATGAKKSNKPNEQTSKRHD 693 KAEPISSSISNMELELNIHNSKAPKKNRLRRKSSTRH-----IHALELVVSRNLSP HSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHER 631 INQGTNQTEQNGQVMNI----TNSGHENKTKGDSIQNEKNPNPIES----LEKESAFKT ---STORCSSKGKTAGLSKGKTHSAASTKYGGESTRNGONIHVLSAEDOCOMETENSVLS IIGAFVTEPQIIQERPLTNKLKRKRRPTSGLHPED-----FIKKADLAVQKTPEM EDVPWITLNSSIQKVNE-WFSRSDEL----LGSDDSHDGESESNAKVADVLDVLNEVDEYS 423 -----EKRAAERHP---LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE 203 SLLEVSTLGK - - - - AKTEP DLTSTHYMGSSSNYASRQPVIAPLDRYAERAVNQVHARNFPSTIATMEASKLCDRRNAGQ -----PAGNLSNKKVTPTASTQHDDENDTENGLDTNMHKTDVC-QHVSEI 514 ----AEDP-----KDL-MLSGERVLQTERSVESSSISLVPGTDYGTQ-----ESI 3.3%; Score 182; DB 1; Length 900; ilarity 18.4%; Pred. No. 1.2e-05; Conservative 142; Mismatches 363; Indels : -----PQGTRDEISLDSAKKAACEFSETDVTNTEHHQPSNN----- NKCVSQCAAFENPKGL-IHGCSK--DNRNDTE 827 -SPAATCGAOFRPGIQAV 783 Indels 382; ----EKYQGSSVSNL Gaps 682 571 531 323 470 420 370 843 743 633 314 269 244 49;

Qy 104 RRWDCSKCLD	0; Conservative 142; Mismatch PAOHQCEHFSIRGYVALLQKKDPKFCSLSR:	Query Match 3.3%; Score 182; DB 2; Length 900; Best Local Similarity 18.4%: Pred. No. 1.2e-05;	; STRANDEDMESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-825-886-20	am	87 71	; ATTOKNEY/AGENT INFORMATION: ; NAME: OSMAN, Richard A ; REGISTRATION NUMBER: 36,627 ; REFERENCE/DOCKET NUMBER: A-59563-3/DJB/RAO		CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/825,886 FILING DATE:	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS . SCETWARE: Patentin Release #1 0 Version #1 30	CITY: San Franc STATE: Californ COUNTRY: USA ZIP: 94111-4187	NUMBER OF CORRESPOND ADDRESSE STREET:	EEE, Ming INVENTION: G	PRIEDMA OSTERME ROWELL, LYNCH,	Application 21328 RMATION: KING, Mary	886-2	Qy 964 STGITSH 970 t t 1 Db 893 KTKSKSH 899	QY 904 SNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVGVLGSLL(;KEIANWSENCGTQSGYKLGV 963 Db 871	Db 828 GFKYPLGHEVNHSRETSIEMEESELDAQYLQNTFKVSKRQSFA 870
RESULT 5 US-08-603-753D-2		QY 904 SNLNGKIPLTFEDLSRHQLHDLHRPLRPHRRVGVLGSLLQKEIANWSENCGTQSGYKLGV 963	OY 844 VVLYPKESMPATHLLRMMDPSTLASFPNYGTSSRNQMESQLHNSQYAHNQYKGSTSTSYG 903	OY 784 DLTSTHVMGSSSNYASROPVIAPLDRYAERAVNOVHARNFPSTIATMEASKLCDRRNAGQ 843	OY 732 SHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAV 783	QY 683 QSTQKELQGHLALTTQESPHPQNFQSTQEQQTHLRMEEMVTIAASSPLF 731	QY 632 QLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTNSQQKSLAS 682	Qy 572 HSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHER 631	Qy 515STQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAEDOCQMETENSVLS 571	Qy 471PAGNLSNKKYTPTASTQHDDENDTENGLDTNMHKTDVC-QHVSEI 514	QY 421 NHTVGEDGLKSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAH 470	Qy 371PVS 420 Oy 371PVS 420	Qy . 315 CEQTCNEPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDAKLCRRKPKK- 370 :: : : : :	QY 276 VAEQCN	QY 216 VAANVSEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETL 275 : : : : : : : : :	QY 157 VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD 215	OY 114KLKTSDNGTAPRTLPAKQNGTSDGCSITFVRSTFVPASVGSQK 156 : : : : :	Db 87 LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146

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Sequence 2
Patent No.
GENERAL II
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: U.S.
FILING DATE: 17 JAN 1995
ATTORNEY AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JE
REGISTRATION NUMBER: 39,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
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ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER,
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TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
NUMBER OF SEQUENCES: 29
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APPLICANT: THOMPSON-BENION, CHERYL L.
APPLICANT: THOMPSON MARILYN E.
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                                                                             FEATURE:
                                                                                                                               CLONE: obtained using POSITION IN GENOME: CHROMOSOME/SEGMENT: ur
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LIBRARY: CDNA
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ORGANISM: Hom
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TISSUE TYPE: female breast
CELL TYPE: ductal carcinoma in situ, invasive
CELL TYPE: breast cancer and normal breast tissue
CELL LINE: not derived from a cell line
ORGANELLE: no
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NAME/KEY: BRCA1 protein LOCATION: 1 to 1863 IDENTIFICATION METHOD: 0 IDENTIFICATION METHOD: 0
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                                                                                                                 MAP POSITION:
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STRANDEDNESS: sir
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btained using published sequence
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KING, MARY-CLAIRE
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observation of mRNA and antisense inhibition of BRCAl gene
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Best Local Similarity
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AUTHORS: Miki, Y., et
 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL: Sc. VOLUME: 266
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DIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDY-----
                               KRHDSDTFP---ELKLTNAPGSFTKCSNTSELKEFVNPSLPREEKEEKLETVKVSNNAED
                                                                                                                         TQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAED-----QCQMETENSV
                                                                                                                                                        AEPISSSISNEL---ELNIMHNSKAPKKNRLRRKSSTRHIHALELVVSRNLSPPNCTELQ
                                                                                                                                                                                                                      AVQKTPEMINQGTNQTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEKESAFKTK
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                                                              LSHSAKVSPAEHDIQI - - -
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US-09-099-753-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,753
FILING DATE: 20 FEB 1996
APPLICATION NUMBER: U.S. 08/373,799
ETLING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     equence 2, Application US/09099753 tent No. 6149903
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMESON, MARILYN E.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND THERAPEUTIC METHODS BASED ON
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
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                                                                                                                                                                                        SOFTWARE: WORD PERFECT 6.1 and ASCII CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: IBM PC/XT/AT compatible OPERATING SYSTEM: Windows 3.1
                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                          CLASSIFICATION:
                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 27707
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                                                                                                                                                                                                                                                                                                                              NORTH CAROLINA
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JENSEN, ROY A.
PAGE, DAVID L.
KING, MARY-CLAIRE
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JETTON, THOMAS L.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: cDNA library
CLONE: obtained using
POSITION IN GENOME:
CHRONOGOUT 'ST
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION: AUTHORS: Miki, Y., et
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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CELL LINE:
                            216 VAANVSEDNTSVDVGALPEVPQ-----ITWHIEVNGADQPPSTPKLSEVVLKRNEDEN 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD: observation of mRNA and IDENTIFICATION METHOD: antisense inhibition of BRCA1 gene OTHER INFORMATION: BRCA1 protein has a negative OTHER INFORMATION: regulatory effect on growth of human mammary cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (919) 419-0383
                                                                                                                                                                                                 87 LKIICAFOLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146
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                                                                                                                                                                                                                                                                                                     48 VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: BRCA1 protein LOCATION: 1 to 1863
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                                                                                              VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD
                                                                                                                                LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE
                                                                                                                                                                -----KLKTSDNGTAPRTLPAKQNGT------SDGCSITFVRSTFVPASVGSQK 156
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                                                                                                                                                                                                                                                                                                                                   3.3%; Score 180; DB ilarity 17.9%; Pred. No. 5.2e Conservative 174; Mismatches
DINTTEKRAAERHPEKYQGSSVSNIHVEPCGTNTHASSIQHENSSILIITKDRM 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEPISSSISNEL---ELNIMHNSKAPKKNRLRRKSSTRHIHALELVVSRNLSPPNCTELQ
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                                                                                                                                                                                                                                       IANWSENCGTQSGYKLGVSTGITSHQMNRKEHFE 979
                                                                                                                                                                                                                                                                                                                        HN-QYKGSTSTSYGSNLNGKIPLTFE----DLSRHQLHDLHRPLRPHPRVGVLGSLLQKE 945
                                                                                                                                                                                                                                                                                                                                                                   EEHSMSPEREMG-----NENIPST------VSTISRNNIRENVFKEASS
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US-08-986-106-2
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Best Local Similarity
Matches 221; Conserv
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APPLICATION NUMBER: 08/60:
PILING DATE: 20 FEB 1996
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: unknown
PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast
TITLE: ovarian cancer susceptibility gene
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 1010: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KING, MARY-CLAIRE
APPLICANT: STEINER, MITCHELL S.
APPLICANT: ROBINSON-BENION, CE
TITLE OF INVENTION: THERAPEUTIC METHODS
TITLE OF INVENTION: PROSTATE CANCER
NUMBER OF SEQUENCES: 26
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204
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                                                                                                                                                                                                                                                                                                 48 VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                        VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD 215
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                                                                                 LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE
                                                                                                            -----KLKTSDNGTAPRTLPAKQNGT------
                                                                                                                                                                     LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146
                                                                                                                                                                                                                                                           IKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQE----STRFSQLVEEL 86
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17.9%; Pred. No. 5.2e-05;
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RESULT 7
US-08-986-106-2
; Sequence 2, Application US/08986106
; Patent No. 6177410
; Patent No. 6177410

GENERAL INFORMATION:
APPLICANT: HOLT,
APPLICANT: JENSEN

HOLT, JEFFREY T. JENSEN, ROY A.

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Sequence 49, Application US/09007678B
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                                                                                                                                                                                                                                                                                                                                                                            DAKKLTWE------QFKATTRNSPAAT-------CG.QFRPGIQAVDLTSTHVMGSS 794
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                                                                                                              IANWSENCGTQSGYKLGVSTGITSHQMNRKEHFE 979
                                                                                                                                                                               HN-QYKGSTSTSYGSNLNGKIPLTFE----DLSRHQLHDLHRPLRPHPRVGVLGSLLQKE
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                                                                                   YKQSLPGSNCKHPEIKKQEYE 1114
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TYPE: PRT

CARNISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1472)

OTHER INFORMATION: Xaa=any amino acid

US-09-007-678B-49 SOFTWARE: MicroSoft WordPad SEQ ID NO 49 Query Match Best Local Similarity Matches 221; Conserv TITLE OF INVENTION: METHOD FOR DETECTION AND TREATMENT OF BREAST CANCER FILE REFERENCE: Attorney Docket No. 6342483 1242-1-2-2 CURRENT APPLICATION NUMBER: US/09/007,678B CUGRENT FILING DATE: 1998-01-15 PRIOR APPLICATION NUMBER: 08/373,799 PRIOR PILING DATE: 1995-01-17 PRIOR PILING DATE: 1995-01-17 PRIOR PILING DATE: 1995-01-14 PRIOR FILING DATE: 1994-01-14 APPLICANT: HOLT, JEFFREY T APPLICANT: JENSEN, ROY A. APPLICANT: PAGE, DAVID L. APPLICANT: OBERMILLER, PA NUMBER OF SEQ ID NOS: 216 VAANVSEDNTSVDVGALPEVPQ-----ITWHIEVNGADQPPSTPKLSEVVLKRNEDEN VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103 AVQKTPEMINQGTNQTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEKESAFKTK TKRKYSDVVDDGSS-----GSVHHTV 468 ADVSDAKLCRRK-----PKKVRLLSEIINANQVEDSRSDEVHRENAADPCED-----LCERKEWNKQKLPCSENPRDTEDVPWITLNSSIQKVNEWFSRSDELLGSDDSHDGESESN 406 NVEK - - - - AEFCNKSKQP - - - - GLARSQHNRWAGSKETCN - - - DRRTPSTEKKVDLNADP GKTEETLVAEQCNLTKDPNPMSGKERDQ-----VAEQCNLTKDPKPVSGQK-----CEQ LLQIT------PQGTRDEISLDSAKKAACEFSETDVTNTEHHQPSNN--VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE -----KLKTSDNGTAPRTLPAKQNGT------SDGCSITFVRSTFVPASVGSQK 156 LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146 RRWDCSKCLD-----IKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQE----STRFSQLVEEL 86 YRKKASLPNLSHVTENLIIGAFVSEPQIIQERPLTNKLKRKRPTSGLHPEDFIKKA-DL AKVADVLDVLNEVDEYSGSSEKIDLLAS--DPHEALICKSDRVHSKSVESDIEDKIFGKT -----DLNTTEKRAAERHPEKYQGSSVSNLHVEPCGTNTHASSLQHENSSLLLTKDRM --DRSTIPVPMEVSMDI------PVSNH-----TVG---EDGLKSSKNK 435 ICNE-----PCEE------VVLKRSSKSKR----KTDKKLMKKQQHSKKRTAQ ROBINSON-BENION, CHERYL L. THOMPSON, MARILYN E. PAGE, DAVID L.
OBERMILLER, PATRICE S. 3.3%; Score 180; DB 4; ilarity 17.9%; Pred. No. 5.2e-05; Conservative 174; Mismatches 387 387; Indels 452; Length 1863; Gaps 464 402 355 346 297 268 244 215 203 113 62;

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US-08-425-061-22
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                                                                                                                                                                                                   APPLICANT: LYNCH, Eric
APPLICANT: SZABO, CSilla
APPLICANT: LEE, Ming
APPLICANT: LEE, Ming
TITLE OF INVENTION: GENETIC MARKERS FO
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                APPLICANT:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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CITY: San Francisco
STATE: California
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                  Version #1.30
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEPAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1202 amino acids
TYPE: amino acid
STEPANDEDNUMES: 61016
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Best Local Similarity
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632 SPPNCTELQIDSCSS---
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                         DEVHRENAADPCEDDRSTIPVPM-----EVSMDIPVSNH-----TVG---EDGL
                                                                                                                                                                                                                                  GKTYRKKASLP---NLSHVTENLIIGAFVTEPQIIQERPLTNKLKRKRRPTSGLHPEDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                ICNE-----PCEE-----VVLKRSSKSKR----KTDKKLMKKQQHSKKRTAQ 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE
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                                ----SEISTORCSSKGKTAGLSKGKTHSAASTKYGGESTRNGONIHVLSAED-----O
                                                                            SAFKTKAEPISSSISNME-
                                                                                                                                                        KKA-DLAVQKTPEMINQGTNQTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DLNTTEKRAAERHPEKYQGSSVSNLHVEPCGTNTHASSLQHENSSLLLTKDRM 297
                                                                                                                 ----KVTPTASTQHDDENDTENGLDTNMHKTDV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.2%; Score 179; DB 1; ilarity 17.9%; Pred. No. 3.1e-05; Conservative 170; Mismatches 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: single
linear
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                                                                            LELNIHNSKAPKKNRLRRKSSTRHIHALELVVSRNL
-SEEIKKKKYNQMPVRHSRNLQLMEGKEPATGAKK
                                                                                                                                                                                                                                                                                                                                                      -----AKLCRRKPKKVRLLSEIINANQVEDSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1202;
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62;

REGISTRATION NUMBER:

36,627

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RESULT 10
US-08-825-886-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1002
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LEE, Ming
TITLE OF INVENTION: GENETIC MARKERS FOR BREAST AND OVARIAN
TITLE OF INVENTION: CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1086 -LG-VLQPEV-----YKQSLPGSNCKHPEIKKQEYE 1114
                            ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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         NAME: OSMAN,
                                                                                                      CLASSIFICATION:
                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                  COUNTRY:
                                                   FILING DATE:
                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NF----EEHSMSPEREMG----NENIPST-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAHSGSLKKQSPKVTFECEQKEENQGKNESNIKPVQTVNITAGFPVVGQKDKP----VDN 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAE-----AP----AP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKCSIKGGSRFCLSSQFRGNETGLITPNKHGLLQNPYRI?PLFPIKSFVKTKCKKNLLEE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSTHVMGSSSNYASRQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKVSNNAED--PKDLM-----LSGERVLQTE-----RS/ESSS-----ISLVPGTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENVFKEASSSNINEVGSSTNEVGSSIN-EIGSSDENIQAELGRNRGPKLNAMLR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y-----ASSVFDTNSQQKSLASQSTQKELQGHL-----ALTTQESPHPQNFQ 707
                                                                                                                                                                                                                                                                     94111-4187
                                                                                                                                                                                                                                                                                                                      SSEE: FLEHR, HOHBACH, TEST, ALBRITTON & T: 4 Embarcadero Center, Suite 3400 San Francisco
                                                                                                                                                                                                                                                                                                     California
                                                                                                                                                                                                                                                                                      USA
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SZABO, Csilla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSTERMEYER, Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KING, Mary-Claire
Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sarah
                                                                                                                                      US/08/825,886
                                                                    08/425,061
                                                                                                                                                                            Version
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                                                                                                                                                                                                                                                                                                                                                              HERBERT
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US-08-825-886-22
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: A-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEPAX: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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TYPE: amino acid
STRANDEDNESS: si
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TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD
                                           SNKPNEQTSKRHDSDTFP--
                                                                                                                                                                                                                                                                                                                                                     KSSKNKTKRKYSDVVDDGSS-----LMNWLN----GKKKRTGSVHHTVAHPAGNLSNK 478
                                                                                                                                                                                                                                                                                                                                                                                                   GKTYRKKASLP---NLSHVTENLIIGAFVTEPQIIQERPLTNKLKRKRRPTSGLHPEDFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVEK----AEFCNKSKQP----GLARSQHNRWAGSKETCN---DRRTPSTEKKVDLNADP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKTEETLVAEQCNLTKDPNPMSGKERDQ-----VAEQCNLTKDPKPVSGQK-----CEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATY--CSVGDQE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRWDCSKCLD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF
                                                                                                                                    SPPNCTELQIDSCSS----
                                                                                                                                                                                                                       SAFKTKAEPISSSISNME-----LELNIHNSKAPKKNRLRRKSSTRHIHALELVVSRNL
                                                                                                                                                                                                                                                                ----KVTPTASTQHDDENDTENGLDTNMHKTDV-----CQHV-----
                                                                                                                                                                                                                                                                                                              KKA-DLAVQKTPEMINQGTNQTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----DLNTTEKRAAERHPEKYQGSSVSNLHVEPCGTNTHASSLQHENSSLLLTKDRM
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                                                                                       CQMETENSVLSHSAKVSPAEHDIQI-----
                                                                                                                                                                           ----SEISTORCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAED-----Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICNE-----PCEE-----VVLKRSSKSKR----KTDKKLMKKQQHSKKRTAQ 355
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                                                                                                                                    --SEEIKKKKYNOMPVRHSRNLOLMEGKEPATGAKK 680
                                                                                                                                                                                                                                                                                                                                                                                                                                              ---EVSMDIPVSNH-----TVG---EDGL
                                                                                       ----MSDLHE----QSLPKKKKKQKLEV
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RESULT 11
US-08-425-061-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: KING,
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                 ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59563-3/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GENETIC THILE OF INVENTION: CANCER NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                    TELEPHONE: (415) 494-8771
                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                      STATE: California
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEHFE 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYGTSSRNQME 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKCSIKGGSRFCLSSQFRGNETGLITPNKHGLLQNPYRIPPLFPIKSFVKTKCKKNLLEE 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSTHVMGSSSNYASRQ---------PVIAPLDRYAE-RAVNQVHAR 821
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SZABO, Csilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KING, Mary-Claire
FRIEDMAN, Lori
OSTERMEYER, Beth
                                                                                                                                                                                                                                               PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENETIC MARKERS FOR BREAST
                                                                                                                                                                                                              US/08/425,061
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                                                                                                                                                                                                                                                 Version #1.30
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 DEVHRENAADPCEDDRSTIPVPM------EVSMDIPVSNH------TVG---EDGL 429
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                                                                                                                                                                                                                                                                                                                                                                SAFKTKAEPISSSISNME------LELNIHNSKAPKKNRLRRKSSTRHIHALELVVSRNL
STQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAE-----
                                       YGTQESISLLEVSTLGKAKTEPNKCVSQCAAFENPKGLIHGCSKDNENDTEGFKYPLGHE
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                                                                                                                   VKVSNNAED--PKDLM-----LSGERVLQTE-----RSVESSS-----ISLVPGTD
                                                                                                                                                         TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD
                                                                                                                                                                                                     SNKPNEQTSKRHDSDTFP---ELKLTNAPGSFTKCSNTSELKEFVNPSLPREEKEEKLET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                KKA-DLAVQKTPEMINQGTNQTEQNGQVMNITNSGHENKTKGDSIQNEKNPNPIESLEKE
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                                                                             -ASSVFDTNSQQKSLASQSTQKELQGHL-----ALTTQESPHPQNFQ
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US-08-825-886-23

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RESULT 12
US-08-825-886-23
US-08-825-886-23
; Sequence 23, Applica
; Sequence 35, Applica
No. 5821328
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                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 23:
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APPLICANT: KING,
APPLICANT: FRIEDM
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino aci
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
            MOLECULE,
                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CITY: San 1
STATE: Cal:
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                          TOPOLOGY:
                                       TYPE: amino acid
STRANDEDNESS: si
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            TYPE:
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                                                                 1363 amino acids
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LYNCH, Eric
SZABO, Csilla
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protein
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                                                                                                                                                                                                                                                                                                                                         Version
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Best Local Similarity
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                                                                                                                                                                                       VKVSNNAED--PKDLM-----LSGERVLQTE-----RSVESSS-----ISLVPGTD
                                                       VNHSRETSIEMEE----
                                                                              STQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAE----
                                                                                                                     YGTQESISLLEVSTLGKAKTEPNKCVSQCAAFENPKGLIHGCSKDNRNDTEGFKYPLGHE
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                                                 -SELDAQYLQNTFKVSKRQSFAPFSNPGNAEEECATF
-QFKATTRNSPAAT------CGAQFRPGIQAVDL
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                              Query Match
Best Local Similarity
Matches 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
                                                                                                                                                                                                                                                          TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD 36,627
REGISTRATION UNMBER: A-58
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LEE, MING
TITLE OF INVENTION: GENETIC MARKERS FOR BREAST AND OVARIAN
TITLE OF INVENTION: CANCER
NUMBER OF SEQUENCES: 24
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                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1852 amino acids
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                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
 48 VDEPAQHQCEHFSIRGYVALL--QKKDPKFCSLSRIFHDQKKCDEHKASSSPFS--VAKF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENVFKEASSSNINEVGSSTNEVGSSIN-EIGSSDENIQAELGRNRGPKLNAMLR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQLHNSQYAHN-QYKGSTSTSYGSNLNGKIPLTFE----DLSRHQLHDLHRPLRPHPRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF-----EHSMSPEREMG-----NENIPST------VSTISRNNIR 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAHSGSLKKQSPKVTFECEQKEENQGKNESNIKPVQTVNITAGFPVVGQKDKP----VDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEHFE
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OSTERMEYER, Beth
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SZABO, Csilla
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                                    Conservative 170;
                                                                                                                                              protein
                                                                                                                                                                                   single
                                  3.2%; Score 179; DB 1; 1
17.9%; Pred. No. 6.2e-05;
ative 170; Mismatches 381;
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                                                                                                                                                                                                                                                                                                                                                      A-59563-3/DJB/RAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                     Length 1852;
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                                    Indels 470;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347
                     822
                                                                                                                                                                                                                                                                                                              666 Y-----ASSVFDTNSQQKSLASQSTQKELQGHL-----ALTTQESPHPQNFQ 707
                                                                                                                                                                                                                                                                                                                                                                                         606 TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD
                                                                                                                                                                                                                                                                                                                                                                                                                               681
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                                                       942 AKCSIKGGSRFCLSSQFRGNETGLITPNKHGLLQNPYRIPPLFPIKSFVKTKCKKNLLEE
                                                                                                                               886 SAHSGSLKKQSPKVTFECEQKEENQGKNESNIKPVQTVNITAGFPVVGQKDKP----VDN
                                                                                                                                                                 744 TEHWG--RKDAKKLTWE-----QFKATTRNSPAAT-----CGAQFRPGIQAVDL
                                                                                                                                                                                                                                                                                                                                                      738 VKVSNNAED--PKDLM-----LSGERVLQTE-----RSVESSS-----ISLVPGTD
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                                                                                                                                                                                                        VNHSRETSIEMEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                             SNKPNEQTSKRHDSDTFP---ELKLTNAPGSFTKCSNTSELKEFVNPSLPREEKEEKLET
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NFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYGTSSRNQME
                                                                                                                                                                                                                                       STQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAE-----AP------
                                                                                                                                                                                                                                                                           YGTQESISLLEVSTLGKAKTEPNKCVSQCAAFENPKGLIHGCSKDNRNDTEGFKYPLGHE
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                                                                                            TSTHVMGSSSNYASRQ----
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                                                                                                                                                                                                        SELDAQYLQNTFKVSKRQSFAPFSNPGNAEEECATF
                                                                              -PVIAPLDRYAE-RAVNQVHAR
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Qy 104 RRWDCSKCLD 113 : 4 :	QY 48 VDEPAQHQCEHFSIRGYVALLQKKDPKFCSLSRIFHD\2KKCDEHKASSSPFSVAKF 103	Query Match 3.2%; Score 179; DB 2; Length 1852; Best Local Similarity 17.9%; Pred. No. 6.2e-15; Matches 222; Conservative 170; Mismatches 381; Indels 470; Gaps 62;	p e	<u>id</u> ::	; TELEPHONE: (415) 494-8700 ; TELEFAX: (415) 494-8771 • ; TELEX: 910 277299 ; INFORMATION FOR SEQ ID NO: 24:	; NAME: OSMAN, Richard A ; REGISTRATION NUMBER: 36,627 ; REFERENCE/DOCKET NUMBER: A-59563-3/DJB/RA) ; TELECOMMUNICATION INFORMATION:	; PRIOR APPLICATION DATA; ; APPLICATION NUMBER: 08/425,061 ; FILING DATE; ; ATTORNEY/AGENT INFORMATION:	о	<pre>#MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30</pre>	; STATE: California ; COUNTRY: USA ; ZIP: 94111-4187 ; COMPUTER READABLE FORM:	; CORRESPONDENCE ADDRESS: ; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT ; STREET: 4 Embarcadero Center, Suite 3400 ; CITY: San Francisco	APPLICANT: LEE, Ming TITLE OF INVENTION: CENETIC MARKERS FOR BREAST AND OVARIAN TITLE OF INVENTION: CANCER NUMBER OF SEQUENCES: 24	OSTERMEYEI ROWELL, Sa LYNCH, Eri SZABO, Csi	; Patent No. 5821328 ; GENERAL INFORMATION: ; APPLICANT: KING, MATY-Claire ; APPLICANT: FRIEDMAN, LOTI		QY 937 VLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEHFE 979	QY 882 SQLHNSQYAHN-QYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVG 936 : : : : : : :	1002
ФУ 882 SQL: : : Db 1033 ENVI	822 1002		Qy 744 ТЕН : 1 Db 886 SAH	Qy 708 STQ Db 837 VNH	Qy 666 Y Db 777 YGTQES	Qy 606 TRE pb 738 VKV	Qy 561 CQM Db 681 SNK	Qy 512 Db 632 SPP	Qy 479 Db 578 SAF	Qy 430 KSS : Db 519 KKA	Qy 389 DEV : Db 462 GKT	Qy 356 ADV Db 407 AKV	Qy 318 ICNE : Db 347 LCERKE	Qy 269 GKT Db 298 NVE	Qy 216 VAA Db 245	QY 157 VSPSTQ : 1 Db 204 LLQIT-	Qy 114 Db 147 LQE	Db. 87 LKI
SQLHNSQYAHN-QYXGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPRVG 936 : :	TIATMEASKICDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYGTSSRNQME	TSTHVMGSSSNYASRQ	TEHWGRKDAKKLTWEOFKATTRNSPAATCGAQFRPGIQAVDL 785	STQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAEAP743 :: :	YASSYFDTNSQOKSLASQSTQKELQGHLALTTQESPHPQNFQ 707	TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD 665	COMETENSVISHSAKVSPAEHDIQIMSDLHEOSLPKKKKKQKLEV 605	SEISTQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAEDQ 560 : :	KVTPTASTQHDDENDTENGLDTNMHKTDVCQHV	KSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGNLSNK 478 : : : ::: :: : : : : : : : : : :	DEVHRENAADPCEDDRSTIPVPMEVSMDIPVSNHTVGEDGL 429 : : : :	ADVSD	ICNEPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQ 355 :	GKTEETLVAEQCNLTKDPNPMSGKERDQVAEQCNLTKDPKPVSGQKCEQ 317 :	VAANVSEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDEN 268	VSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAE-ANTDSPMKDLQGPAQNYD 215	KLKTSDNGTAPRTLPAKQNGTSDGCSITFVRSTFVPASVGSQK 156 :: : LQETSLSVQLSNLGTV-RTLRTKQRIQPQKTSVYIELGSDSSEDTVNKATYCSVGDQE 203	LKIICAFQLDTGLEYANSYNFAKKENNSPEHLKDEVSIIQSMGYRNRAKRLLQSEPENPS 146

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RESULT 15
US-08-480-784-2
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; MOLECULE TYPE: US-08-480-784-2
                                                                                                                  APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
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APPLICANT: Skolnic
APPLICANT: Goldgar
APPLICANT: Miki, Y
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                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILLING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILLING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILLING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILLING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILLING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1863 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer TITLE OF INVENTION: Susceptibility Gene NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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APPLICANT:
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CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
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                                         TOPOLOGY:
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Shattuck-Eidens, Donna M.
Tavtigian, Sean V.
Wiseman, Roger W.
Futreal, P. Andrew
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                                         linear
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Query Match Best Local Similarity

3.2%; 17.9%;

Score 179; DB 1; Pred. No. 6.2e-05;

Length 1863;

886 SAHSGSLKKQSPKVTFECEQKEEN 786 TSTHVMGSSSNYASRQ 1
QY 708 STQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAEAP
QY 666 YASSVFDTNSQQKSLASQSTQKELQGHLALTTQESPHPQNFQ
QY 606 TREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSD
Qy 561 CQMETENSVLSHSAKVSPAEHDIQIMSDLHEOSLPKKKKKQKLEV
Qy 512SEISTQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAED
Qy 479KVTPTASTQHDDENDTENGLDTNMHKTDVCQHV
Qy 430 KSSKNKTKRKYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGNLSNK :
Qy 389 DEVHRENAADPCEDDRSTIPVPMEVSMDIPVSNHTVGEDGL
Qy 356 ADVSDAKLCRRKP
Qy 318 ICNEPCEEVVLKRSSKSKRKTDKKLMKKQOHSKKRTAQ :
Qy 269 GKTEETLVAEQCNLTKDDPMSGKERDQVAEQCNLTKDPKPVSGQKCEQ :
Qy 216 VAANVSEDNTSVDVGALÞEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDEN : : : : : : : : :
Db 204 LLQIT
147
Qy 114KLKTSDNGTAPRTLPAKQNGT-
Qy 104 RRWDCSKCLD
Db 31 IKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQESTRFSQLVEEL
Matches 222; Conservative 1

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Title:
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Copyright (c) 1993 - 2000 Compugen Ltd
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	SLSRIFHDQKKCDEHKASSSPFSVAKFRRWDC 108	SEE	QKKDPKF ::: : RERDLRK	QCEHFSIRGYVALLQKKDPKFC:	QCEHF : : KCDHF	25	Ωy
58;); DB 2; Length 1096; 1.7e-13; ches 403; Indels 348; Gaps	; Score 393; I ; Pred. No. 1.7 189; Mismatches	7.1% 21.0% tive	Similarity); Conserva	y Match Local S hes 250	Query Ma Best Lo Matches	X 111 O
	stical protein F15N18.120	49/1; 569/3 lana hypothet	/1; 1 thal	n: 5 //2; 91/1; 131, 8.120 : Arabidopsis	position: cons: 32/2 e: F15W18. erfamily:	Map posi Introns: Note: F1 Superfam	C A A A A A A A A A A A A A A A A A A A
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3	April 2000	, M.; HOIZER Ce Database,	Sequence	m.; Hilbert, H. d to the Protein nce number: Z244 ion: T48512	nce nu ion: T	evan, mitted mitted eferen ccessi	Sub A; R
	S . Drupat A . Depatorhooft	. uolac	0	48512	, U	ccession:	C; A
	sis thaliana · cress) Apr-2000 #text_change 05-May-2000	20 - Arabidopsis na (mouse-ear cr revision 20-Apr	n F15N18.120 sis thaliana #sequence_r	al protein F15 Arabidopsis t -Apr-2000 #seq	O (i	RESULT T48512 hypothetic C;Species C;Date: 20	RES T48 hyp C;S
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natural killer cell tumor-recognition protein - mouse
N.Alternate names: cyclophilin-related NK-tumor recognition protein; natural kil
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1994 **sequence_revision 17-Jul-1994 **text_change 05-Nov-1999
C;Accession: B47328; I77662
R;Anderson, S.K.; Gallinger, S.; Roder, J.; Frey, J.; Young, H.A.; Ortaldo, J.R.
Proc. Natl. Acad. Sci. U.S.A. 90, 542-546, 1993
A;Title: A cyclophilin-related protein involved in the function of natural kille
A;Reference number: A47328; MUID:93133824
A;Accession: B47328
A;Status: preliminary
A;Rolecule type: mRNA
A;Residues: 1-1507 <AND>
A;Rors-references: GB:L04289; NID:912866
A;Note: authors translated the codon AGT for residue 972 as Arg
R;Rinfret, A.; Anderson, S.K.
A; Accession. A; Accession A; Accession A; A; Accession E type: mRNA A; Residues: 1-1507 < AND> A; Cross-references: GB:L04289; NJ A; Note: authors translated the constraint A; Anderson, S.K.
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A,Gene: NK-TR
C;Superfamily: natural killer cell tumor-recognition
C;Keywords: alternative splicing; lymphocyte
F;60-230/Domain: cyclophilin homology <CYP>
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A;Title: II-2 regulates the
A;Reference number: I57820;
A;Accession: I77662
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                  QQKSLASQSTQKELQGHLALTTQESPHPQNFQSTQEQQTHLRMEEMVTIAASSPLFSHHD
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                                                                                               IPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTNS
                                                                                                                                        SKYVRGREKSSRHRKYSESRSSLDYTSDSDQSHVQVYSAPEKEKQGKVEALNDKQ-----
                                                                                                                                                                                                                       SPSSRSHSPNKYSDGSQHSRSSSYTSVSSDDGRRAMFRSNRKKSVTSHKRHRSNSEKTLH
                                                                                                                                                                                                                                                            --- GKTHSAASTKYGGESTRNGQNIHVLSAEDQCQMETEN---SVLSHS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEQNIPDVAPVVSDQKPSVSKSGRKIKGRGTIRYHTPPRSRSHSESKDDDSSETPPHWKE
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Pred. No. 0.00031;
9; Mismatches 459
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A;Title: Prediction of the coding sequences of unidentified human genes. X. The comple A;Reference number: 214142; MUID:98403880
A;Accession: T00385
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C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision
C;Accession: T00385
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                                                                           KGPLPFLINRAMSCPSGEPHASTGREGRKKPLTSGMDASELTFRAWERIISPVESDSS--
                                                                                                           VGALP-----EVPQITWHIE------VNGADQPPSTFKLSEVVLKRNEDENGKT
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QCLAFLENVKRS---LTQGRLWKPSFLKNPG-----FLKDDL----RNP
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                                  WNALQLGSVSSSADFLSARNSIAQSWTRGKGKMVHPLDRFVRQDICITNKNP 1041
                                                                     SELPSCD--GN-----ESWAYRSGTKTGPRSAISI-----YRPIDYGIFGKE
                                                                                                      RPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEHFEALNSGMFSAK
                                                                                                                                        NVHGDLLRKS-----HPPKVRERHFSESTSI---DNALSRLTLGNEFSVNNGYSRRFRSF
                                                                                                                                                                          PNYGTSSRNQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPL
                                                                                                                                                                                                            -AQK-----SRVSSPLASFLQQQRSASSL----EWEPEPHLYR---SKSLKSI
                                                                                                                                                                                                                                                                                                                KDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIAPLDR 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -NKTLSHSESQVFALTPALHKLQLGEETQSDEPNLESLQSEPRELPQRSQEANMTESRK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRSSWECTGSGRAIPFTGSGKCPQKDHTSTAVGDGSSGSQPREGRG----DIGTNCQKMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EISTORCSSKGKT----AGLSKGKTHSAASTKYG--GESTRNGONIHVLSAEDOCQMET
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                                                                                                                                                                                                                                                                              -VTAAQNLVRESGAP-----SPITFTSLREAEFSDNQRRLSPPF-PLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -AEDEMQKSAWDQPSLPEGNK--NKTNLDD---LVKGENRSSVKHRLA
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RESULT 4
$62982
vacuolar protein VAC7 - yeast (Saccharomyces cerevisiae)
vacuolar protein VAC7 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein N2467; protein YNLO54w
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 07-May-1999
C;Accession: $63982; $58722; $68168
R;Bergez, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: $62975
A;Accession: $62975
A;Accession: $62982
A;Molecule type: DNA
A;Residues: 1-1165 <BER>
A;Cross-references: EMBL:Z71330; NID:g1301918; PID:e239893; PID:g1301921; MIPS:YNLO54
A;Experimental source: strain $288C
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R;Bergez, P.; Dolgnon, K.; CIULZEC, ...
Yeast 12, 297, 1996
A;Title: Corrigendum to: the sequence of a 44 458 bp fragment located on the left arm A;Reference number: S68168; MUID:97060022
A;Accession: S68168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 14L
C;Function:
A;Description: required for normal vacuole inheritance and
C;Keywords: transmembrane protein; yeast vacuole
E;925-941/Domain: transmembrane #status predicted <TMN>
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1001 <BEW>
A; Residues: 1-1001 <BEW>
A; Cross-references: EMBL: U12141
A; Mote: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
A; Mote: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
A; Bergez, P.; Doignon, F.; Crouzet, M.
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A;Cross-references: SGD:S0004999; MIPS:YNL054W
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A;Residues: 1-1165 <BEF>
A;Residues: 1-1165 <BEF>
A;Cross-references: EMBL:U12141; NID:g1314216; PID:g1098487
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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Yeast 11, 967-974, 1995
A;Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome A;Reference number: S58711; MUID:96021608
A;Accession: S58722
A;Status: nucleic acid sequence not shown; translation not shown
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473 QQQQPPKQQQQQNHGITSKISAPLLNNNKKLLSRLKNSKHISTGAILNNTIATISTNPN 532
                                                          629 HERQLMTETDCSDINRIQSKTTA---DDDCVIVAAKDGSIXYAS-----SVFDTNSQ 676
                                                                                                                       414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 HIGSVSST-NNNSNNALINHNPLSSH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 NYDVAANVSE-----DNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNED 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 QKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNJAAEANTDSPM--KDLQGPAQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 TANTTSNVVQHNLPTIDNNLMDSDATSH-NQDHWHSDIN.XAGTSMST---SDIPTDLHLE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 RKLTVETETVEAPVANNLLL-----SNNSNVVAPNPST?SASTST-SPLHREIVDDSVA 58
                                                                                                                                                                                                                                                                                                                                                                       PTASTQHDDENDTENGLDTNMH-----KTDVCQHVSEISTQRCSS------KGKTA 526
                                                                                                                                                                                                                            SVSSSNADNHNNNKKKTSSNNNGNNSNSASNKTNADIKN;;NADLSASTSNNNAIND----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLKSSKNKTK---RKYSDVVDDGSSLM--NWLNGKKKRT3SVHHTVAHPAGNLSNKKV-T 481
                                                                                                               -DSHESNSEKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQ
                                                                                                                                                                       SDLHEQSLPKKKKKQ-----KLEVTREKQTMIDDIPMDIVELL-----AKNQ 628
                                                                                                                                                                                                                                                                              GLSKGKTHSAASTKYGGESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAEHDIQIM 586
                                                                                                                                                                                                                                                                                                                                      PNHSNADDNENNNKMKKNKNINSGKNERNDDTSKICTTS!!KTAPSTAPLGSTDNTQALTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSANIHGPSSTSASKAFRKASAFSNNTAPSTSNNIGSNT:PAPL----LPLPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LSNPSSSLRNKKSSLLVASN------PAFASDVELSKKKPAVISNNMPTSNIALYQTA 191
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	Db 533 LNSNVMQNNNNLMSGHNHLDELSSIKQEPPH-	QLQQQQPPM
	Qy 732 SHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATC-	QFKATTRNSPAATCGAQFRPGIQAVDL 785
	Db 586DSNVIAKSPDKRSSLVSLSKV	PDKRSSLVSLSKVSPHLLSSTSSNGNTISCPNVATNSQELEPNNDI 639
	Qy 786 TSTHVMGSSSNYASRQ-	ER 813
	Db 640 STKKSLSNSTLRHSSANRNSNYGD	STKKSLSNSTLRHSSANRNSNYGDNKRPLRTTVSKIFDSNPNGAPLRRYSGVPDHVNLED 699
	Qy 814 AVNQVHARNFPSTIATMEASKLCD	AVNQVHARNFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLLRMMDPSTLASFPNYG 873
	Db 700 YIEQPHNYPTMQNSVKKDEFYNSRN-	NKFPHGLNFYGDNNVIEEENNG 746
	Qy 874 TSS	NOMES
	Db 747 DSSNVNRPQHTNLQHEFIPEDNES	DSSNVNRPQHTNLQHEFIPEDNESDENDIHSMFYYNHKNDLETKPLISDYGEDEDVDDYD 806
	Qy 892NOYKGSTSTSYGSNLNGKIPL-	TFEDLSRHQLHDLHRPLRPHPR 934
	Db 807 RPNATFNSYYGSASNTHELPLHGRMPSRSNNDYYDFMVGNNTGNNNQLNE-	RSNNDYYDEMVGNNTGNNNQLNE-YTPLRMKRG 865
	Qy 935 VGVLGSLLQKEIANWSENCG	TQSGYKLGVSTGITSHQM-NRKEHFEALNSGMFSA 988
	Db 866 QRHL-SRTNNSIMNGSIHMNGNDD	SRTNNSIMNGSIHMNGNDDVTHSNINNNDIVGYSPHNFYSRKSPFVKVK 918
	QY 989 KWNALQLGSVSSSADFL	ADFLSARNSIAQSWTRGKGKMVHPLDRFVRQDIC 1035
	Db 919NFLYLAFVISSLLMTGFILGEL	ILGFLLATNKELQDVDVVVMDNVISSSDELIFDIT 970
	QY 1036 ITNKNPADET 1045	
	Db 971 VSAFNPGFFS 980	
	RESULT 5 T34513 hypothetical protein ZK783.1 - Caenorhabo C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 2: C;Accession: T34513	Caenorhabditis elegans ns evision 29-Oct-1999 #text_change 29-Oct-1999
	R; Favello, A.; Vandin, M. submitted to the EMBL Data Library A; Description: The sequence of C., A; Reference number: Z21536	August 1994 Alegans cosmid ZK783.
	A;Status: preliminary; translated A;Molecule type: DNA	m GB/EMBL/DDBJ
		:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1 N2; clone ZK783
	A; Map position: 3 A; Introns: 14/1; 48/2; 84/1; 196/3; 3504/1	03/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/
	Query Match Best Local Similarity 17.9%; I Matches 242; Conservative 179	Score 215.5; DB 2; Length 3507; Pred. No. 0.0031; 79; Mismatches 510; Indels 419; Gaps 52;
	Qy 12 RVVGTNCMLARGGTGAVAPVLELTATPRQDAAA-	RQDAAAEAGVDEPAQHQC- 56
	Db 1780 RMGSCGCKCMAGYTGDGATCIKIE	SCGCKCMAGYTGDGATCIKIEEEPKSDKTACTDEWSRLCELEKKQCTVDEEEVPQCG 1839
	Qy 57EHFSIRGYVALLQ	
٠	Db 1840 ACLPGHHPINGTCQSLQISGLCAQI	INGTCQSLQISGLCAQKNDCNKHAECIDIHPDSHFCSCPDGFIGDGMICDDV 1899

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                                                                                                                                                                                              APLDRYAERAVNQVHARN--
                                                                                                                                                                                                                                              ATTRNSPAATCGAQ------FRPGIQAVDLTSTHVMGS-----SNYASRQPVI
                                                                                                                                                                                                                                                                                               TVTSSEPSESTKRTTVSTTVSTTT
                                                                                                                                                                                                                                                                                                                                                          KPSQEPAGILTSTVVVPTSSVSLITASEIEAITSNTPFKQGRTPITTSPKSLVKSTTSPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHKTDVCQHVSEISTQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHVLSAEDQC
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                                RLITGTPDDLIVSVTVPSHGNRRQNITASSVPSNSTSPIILPSESLTTPQPPPTTTTTAK
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                                                                                                                            ----RNAGQVVLYPKESMPATHLLRMMDPS--TLASFPNYGTSSRNQMESQLHNSQY---
                                                                                                                                                              APAVTVSSEASSTTLEENSSTSSPTSSEASVKLSSLFPESI-TSEAVTVSSRAPAEITMS
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LHDLHRPLRPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGVST
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A;Accession: T13U3U
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R;Lantz, V.A.; Miller, K.G.
J. Cell Biol. 140, 897-910, 1998
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EQELQQLQSKSAESESALKVVQV-QLEQLQQQAAA-----SGEEGSKTVAKLHDEISQ
                                                          PMDIVELLAKNQHERQLMTETDCSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTNSQ
                                                                                                                                                                                                                                                                                              QHVSEISTQRCSSKGKTAGLSKGKTHSAAS-TKYGGESTRNGQNIHVLSAEDQCQMETEN
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9; Mismatches 35
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proliferation potential-related protein - mouse C; Species: Mus musculus (house mouse) C; Date: 11-Jan-2000 #sequence_revision 11-Jan-20(0 C; Accession: T42727 R; Witte, M.M.; Scott, R.E. submitted to the EMBL Data Library, November 1996 A; Accession: T42727 A; Accession: T42727
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A;Molecule type: mRNA
A;Residues: 1-1560 <NIT>
A;Cross-references: EMBL:U83913; NID:g3858884; PID:g3858885; PIDN:AAC72432.1
A;Experimental source: strain Balb/C
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C;Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                            DQKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKTSDNGTAPRTL---PAKQNGT-----
                                         VKKDCSKDIKSEKPASKDEKAKKPEKNKLLDSKGEKRKFKTEEKSVDKDFESSSMKISKV
                                                                              CEQICNEPCE-
                                                                                                                                             KLSEVVLKRNEDENGKTEETLVAEQCNLTKDPNPMSGKFRDQVAEQCNLTKDPKPVSGQK
                                                                                                                                                                                   SATAKKDNVLKPSKGPQEKVD----
                                                                                                                                                                                                                  AAEANTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGALFEVPQITWHIEVNGADQPPSTP 254
                                                                                                                                                                                                                                                                                       SDGCSITFVRSTFVPASVGSQKVSPSTQSSQGKNADRSILPKSVQEGNDSKCNAPSGKNG
                                                                                                                                                                                                                                                                                                                          NEEKGEESESFLNPELLGKFRKCRGSSGIDETKTD-----TLFVFPSREDATPVRDEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSTGTQTTIKDLQERLEITNAELQHKEKMASEDAQKIALLKTLVEAIQVANANISA 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENCGTQSGYK-LGVSTGITSHQMNRKEHF---EALNSGNFSAKWNALQLGSVSSSA 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPHPF.VGVLGSLLQKEIA-----NWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QAVDLTSTHVMGSSSNYASRQPVIAPLDRYAERAVNQVIA-----RNFPSTIATMEASKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWE(FKATTRNSPAATCGAQFRPGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EETQAA----LSSYHTD-----
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                                                                                                            -----LKKAKEEATKIDS--VKPSSSSQKD-EKVTGTFRKAHSKSAKEHQEAKPAKDEK
-QHSKKRTAQADVSDAKLCRRKPKKVRLLSEIINANQVEDSRSDEV---HRENAA
                                                                                                                                                                                                                                                                                                                                                                                               Conservative 150;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 213.5; IB
Pred. No. 0.0014;
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                                                                          -EVVLKRSSKSKFKTDKKLMKKQ------
                                                                                                                                                                                                                                                      -KSVSDKDKREKEKPKVKSDKTKRK----SDG
                                                                                                                                                                                 -----GDRHKSPR-----SEPP---
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                                                                                                                                                                A; Introns: 34/3;
                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                       A;Cross-references: EMBL:AL049607; GSPDB:GN00062; ATSP:F11C18.80 A;Experimental source: cultivar Columbia; BAC clone F11C18
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                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                     A; Gene: ATSP:F11C18.80
                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-852 <BEV>
                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: T06310
                                                                      Query Match
Best Local S
Matches 174
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                                                                      nes 174;
                                31 VLELTATPRO-----DAAAEAGVDEPAQHQCEHFSIRGY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---GKDSSGGKLPCILNPPDLPMEKELAVGQVEKSAVKPKPQLSHSSRLSSDLTRETDEA 1405
ILETVAKVRSCVVMLDLECDALLIEMFQHFLK--AIRDHHSGNVFSSMENIMTLVLEESE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSVSPSRSHSPSGSQTRSHSSSASSAGSQ~DSKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPLRPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFEPDYNESDSESNVSVKEEEAVASISKDLKEKTTEKAKESLTVATASQPGADRSQSQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDHKAPYETKRPCEE--TKPVDKISGKEREKHAAEARN-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --HDDQYIAEAPTEHWGRKDAKKLTW---EQFKATTRNSPAATCGAQFRPGIQAVDLTST 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSKRRDERGELA-RRKDSP-PRGKESLSGQKSKLREERDLPKKGAESKKSNSSPPRDKKP
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                                                                    h 3.8%;
Similarity 21.2%;
74; Conservative 97
                                                                                                                                                                102/3;
                                                                                                                                                                                                                                                                                                                                   Z15589
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                                                                                                                                                                163/2; 205/3; 269/3; 282/3; 564/3; 602/3; 622/2;
                                                                        97;
                                                                    Score 209.5; DB 2;
Pred. No. 0.001;
7; Mismatches 282;
                                                                      Indels
                                                                                                         Length
                                ----VALLQKK 71
                                                                        269;
                                                                      Gaps
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                                                                                                                                                                639/3;
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Indels Length

Gaps

52;

1295; 339;

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hypothetical protein T06E4.1 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T24587 R;Lloyd, C.
                                              A:Molecule type: DNA
A;Residues: 1-1295 <MIL>
A;Cross-references: EMBL:Z70756; PIDN:CAA94789.1; GSFDB:GN00023; CESP:T06E4.1
A;Experimental source: clone T06E4
C;Genetics:
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A; Introns: 17/3;
                A;Gene: CESP:T06E4.1
A;Map position: 5
                                                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z19910 A; Accession: T24587 A; Status: preliminary; translated fi
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218/2; 385/3; 481/3; 946/3; 1034/3; 1222/2
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940	MNKEMVDELNAKLGDALEGMEELKKSLEVSEAKV	907	뫄
972	PLRPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQM	913	Qy
906	NSSHKRDMVALASQLEELQHKLVVGESQVENVKEELIGAKI	866	Db
912	PATHLLRMMDPSTLASFPNYGTSSRNOMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPL	853	Оу
865	EEIKQLQLDLQNFKQNAEVLESLNEKL	839	Db
852	SSSNYASROPVIAPLDRYAERAVNOVHARNFPSTIATMEASKLCDRRNAGOVVLYPKESM	793	οу
838	QEVSRSVVDAAVQEKDGLLRLVDTLKLKIEDTEKSAQDLQQSSV	795	DЪ
792	HHDDQYIAEAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMG	733	Qy
794	DDLKEKLHSAESTNQELQVSLEMLKIEVSNARQKVMESEVLKESFEALQLELSAS	740	рb
732	STOKELOGHLALTTQESPHPQNFQSTQEQQTHLRMEEMVTIAASSPLFS	681	Qy
739	DSIQAEVRVQSDSAADQKHILEDYLRKIRQAEETNEKLRSDLASSEEQILDLKNQQESLI	680	Db
089		644	Qy
679	EDCQKLRDQLKEEQIQQLVSLRETSEVMHQESARHQEEKYQIQSKLMSTEAEVIELRSSI	620	ДĎ
643	HERQLMTETDCSDIN	809	Qy
619	SVDKVCSLQLELEEIQHETSVELEEAEIRIKELELAQEEAVKTGSSQLKKLEIVQ	565	рb
607		551	Qy
564	SESTQUEYSLALENTVSELETMRREYKA	537	Db
550	TAGLSKGKTHSAASTKYGGESTRNGQ	491	Qy
536	ELLEQINSLRVENAKLVDMEGQLNDAHRKAEDKDVRISELLTTIESLRQDSEASDKLLMD	477	В
490	TPTASTQHDD	449	Qy
476	MSALQPKNDTTELEELQKTLDDLKIDCCNLTSKMLELQSELVEVKEKATSEIGEAVQKNG	417	Db
448		397	Qy
416	CKAKEDIETLOMKYVELETTINKEVFSNSEIETLKSEHEIVRKLMLDEIHRLENE	362	망
396	RTAQADVSDAKLCRRKPKKVRLLSEIINANQVEDSRSDEVHR-ENA	352	Qy
361	KLQFEHQLEELKSRCEELTDKALKVDVMQHSIEDYEKKFVELQEMKEEADEQL	309	рь
351		294	Оу
308	EIKEAREVEEKMLMQQVEEAVKKTKSEREAAKTLEQLLEKRIEELEMKLT-EPNGE	254	Db
293	DPNPMSGKE	243	Qy
253	VQSTSVESVQSTSQHEKSRIEYSLYEFEMLEKNIEHDEVVKDLQLKIELLGEKHRQTL-V	195	В
242	NTDSPMKDLQGPAQNYDVAANVSEDNTSVDVGALPEVPQITWHI	199	Qy
194	PIESEV	146	рь
198		143	Qy
145	DNSVCEPPRASSAHDVDPNLEQTKVYSEDSISKDCSIADESFATDG-DVTL	96	DЪ
142	DQKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKT-SDNGTAPRTLPAKQNGTSDGCSITF	84	Qy

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A; Molecule type: mRNA
A; Residues: 1-1630 <WUA>
A; Cross-references: GB:006746
C; Keywords: glycoprotein
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J. Biol. Chem. 269, 11950-11955, 1994
A;Title: Molecular cloning and sequencing
A;Reference number: A33577, MUID:94216302
A;Accession: A53577
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                                                                   TQRCSSKGKTAGLSKGKTHSAASTKYGGESTRNGQNIHV1.SA--EDQCQME-TENSVLSH
                    SAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTHIDDIPMDIVELLAKNQHERQ
                                              TQETSTQELTS -- SQSQHTGSMKTTHNPQTTRNTEVTTT1.SASSSDQVQVETTSQTTLSD
                                                                                                      TSHAPSVSSSSPSPPSTEGTSVDTGLTTAVTTQDSTPAT::QGSLTSSSQTLSTVSPLSTS
                                                                                                                                                                                      ----SNHTVGEDGLKSSKNKTKRKYSDV----VDDG;3SLMNWLNGKKKRTGSVHHTV
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                                                                                                                                                                                                                                                                       QHTGIMKTTSRTQTTTPTEVTTRTLSASSSDHRQAETSS;\TTLSPDTTTTSHAPRESSPP 358
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Pred. No. 0.0023;
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A; Variety: strain Z29
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 02-Jun-2000 C; Accession: T44231
C; Accession: T44231
C; Accession: T46231
C; Accession: 
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A; Restidues: 1-1520 < DOM>
A; Cross-references: EMBL: AF157706; PIDN: AAD49674.1
A; Experimental source: strain Z29; variant B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Human herpesvirus 6B genome sequence: A;Reference number: Z22734; MUID:99412318 A;Accession: T44231
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SGQKCEQICNEPCEEVVLKRSSKSKRKTDKKLMKKQQHSKKRTAQADVSDAKLCRRKPKK 370
                                                                                                                  NFAVHKTKIHSDSELHHTKKNIHRSKTSL--QDRVLISKHAPRAPTKDNSYKKHHDPKDT
                                                                                                                                                                                                                                    SEVVLK---RNEDENGKTEETLVAEQCNLTKDPNPMSGKERDQVAEQCNLTK---DPKPV 310
                                                                                                                                                                                                                                                                                                                                                      --RSDLKQRKS-NQHEDEAVTEARDFSKLDPLLSPLPMTPE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TQKYKKTHIRCR-----SIQKTKGHSS--QTINKHKVQKHNEN--HVPS-----
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Pred. No. 0.0028; 
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N;Alternate names: hypothetical protein EG:49E4.1
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-1
C;Accession: T13564
R;Spanos, L.; Papagiannakis, G; Siden-Kiamos, I.; Louis, C.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila mela, Reference number: 217689
A;Reference number: 217689
A;Recession: T13564
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Residues: 1-5327 <SPA>
A;Residues: 1-5327 <SPA>
A;Cross-references: EMBL:AL031128; PIDN:CAA20006.1
C;Genetics:
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A;Cross-references: FlyBase:FBgn0025392
A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5:
A;Note: EG:49E4.1
C;Superfamily: Drosophila 576K microtubule-associated protein homolog
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     FKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIAPLDRYAERAVNQVH
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                                            SRRESVVESSKDDAEKSESRPESVIASGEPV-
                                                                               SPHPQNFQSTQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQ
                                                                                                                                                                                             ASRPPSVVESTKADSTKGDISPSPESVLEGPKDDVEKSKESSRPPSVSASITGDSTKDVS
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-RPGSVVESVTAE---DEKSEQQSRRESVAESVKADTKKDGKSQ

ρ γ _ν	29 ARNFPSTIATMEASKLCDRRNAGQVVLYPKESMPATH:LRMMDPSTLASFPNYGTSSR 877	
Ωy	878 NQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRHQLHDLHRPL	
용	2878	
Qγ	930 крнрк	
문	2930SVVG	
VΩ	990 WNAL	
Ъ	Db 2974VLGSLKDEGDKTTSRRVSVADSIKDEKSLLV 3004	
RESU T344 hypo	RESULT 13 T34418 hypothetical protein F12F3.3 - Caenorhabditis elegans	
C; Da	#sequence	
R; Fu Subm A; De	R.Fulton, B.; Wohldmann, P. submitted to the EMBL Data Library, July 1998 A.Description: The sequence of C. elegans cosmid @12F3. A.Beference number: Z21521	
A; Ac A; St	A;Accession: T34418 A;Status: preliminary; translated from GB/EMBL/DD3J A;Molecule type: DNA	
A; Ex	A; RESIQUES: 1-3488 <ful> A;Cross-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3 A;Experimental source: strain Bristol N2; clone F12F3</ful>	
A; Gei	Gene: CESP:F12F3.3	
Qu Be Ma	Query Match 3.7%; Score 204; DB 2; Length 3488; Best Local Similarity 18.5%; Pred. No. 0.013: Matches 214; Conservative 161; Mismatches 419; Indels 364; Gaps 46	
₽ 2		
B 5	DV 85QKKCDEHKASSSPFSVAKFRRWDCSKCLDKLKTSDNG:RAPRTLPAKQNGT 134	
Ωy	135	
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Ωy	277 AEQCNLTKDENPMSGKERDQVAEQCNLTKDEKFVSGQKC;;QICN	
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٧	22 PCEEVV	

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1476	ETKSKQTEEAPKESVDEKPKKKVLKKKTEKSDSSISQKSKSAKSTVDAAETLESDENLVE	1417	당
837	NYASRQPVIAPLDRYAERAVNQVHARNEPSTIATMEAS-KLCD	796	Qy
1416	KADAEKLKLEEQKKKAAEIALIEIQKEQEKLAQEQSRLEDEAKKSAEKQKLES	1364	В
795	WGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSS	747	Qy
1363	EKDEQLKLDTEAASKKAAAEKLELEKQSHIKKAAEVD-AVKKQKELEEKQRLESEAATK-	1306	Ф
746	ELQGHLALTTQESPHPQNFQSTQ-EQQTHLRMEEMVTIAASSPLFSHHDDQYIAEAPTEH	688	Qу
1305	PSESETQKVADAARKQKETDEKQKLEAEITAKKSADEKSKLEAESKLKKAAEVEAAKKQK	1246	Дb
687	DGSDYASSVFDTNSQQKSLASQSTQK	662	Qy
1245	TA-EKQTKLEKDEKSTKESESKETVDEKPKKKVLKKKTEKSDSSISQKSETSKTVVESAG	1187	ф
661	NQHERQLMTETDCSDINRIQSKTTADDDCVIVAAK	627	Qy
1186	KKAAGADAVKKQKELDEKNKLEANKKSAAGKLKIEEESAAKSKQTVEEQAKLD-AQTKAK	1128	Db
626	MSDLHEQSLPKKKKKQKLEVTRE	586	Qy
1127	TKKASADKLKLEEQAQAKKAAEVEAAKKQKEKDEQLKLDTEAASKKAAAEKLELEKQAQI	1068	Дβ
585	TKYGGESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAEHDIQI	539	Qy
1067	KETDEKLKLDAEIAAKTKQEADEKSKLDAQEKIKKVSEDDAARKEKELN-DKLKLESEIA	1009	B
538	DENDTENGLDTNMHKTDVCQHVSEISTQRCSSKGKTAGLSKGKTHSAAS	490	Qγ
1008	DETPKKKIIKKKTEKSDSSISQKSATDSEKVSKQKEQDEPTKPAVSETQMVTEADKSKKQ	949	В
489	WLNGKKKRTGSVHHTVAHPAGNLSNKKVTPTASTQHD	453	Qy
948	ADKLKLEEESAAKSKKVSEESVKFGEEKKTKAGEKTVQVESEPTSKKTIDTKDVGATEPA 948	889	В
452		408	Qy
888	QKEKDEQLKLETEVVSKKSAAEKLELEKQAQIKKAAEADAVKKQKELNEKNKLEAAKKSA	829	Дb
407	CRRKPKKYRLLSEIINANQVEDSRSDEVHRENAADPCEDDRSTI	364	Qy
828	PAESEAQKIAEVNKAKKQKEVDDNLKREAEVAAKKIADEKLKIEAEANIKKTAEVEAAKK 828	769	В

RESULT 14

F90073

hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)

C;Specles: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C;Accession: F90073

R;Kuroda, M,;Ohta, T.; Uchiyama, I.; Baba; T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: F90073

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2271 <KUR>
A;Cross-references: GB:BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:GN00149
A;Experimental source: strain N315 A; Gene: SA2447.

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SDSKSTSGSTSTSGSLSTSTS-LSGSESVSES
                                 LNSGMFSAKWNALQLGSVSSSADFLSARNSIAQS 1014
                                                                                                                                                                             MDPSTLASFPNYGTSSRNQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPLTFEDLSRH
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                                                                                                                                                                                                                                                                                                                      EAPTEHWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASR
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                                                                                                      QLHDLHRPLRPHPRVGVLGSLLQKEIANWSENCGTQSGYKLGVSTGITSHQMNRKEHFEA
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RESULT 15
B71609
hypothetical protein PFB0680w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: B71609
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, I
R; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith,
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
A;Accession: B71609
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Residues: 1-665 <GAR>
A;Cross-refrences: GB:AE001410; GB:AE001362; NID:g3845245; PIDN:AAC71925.1; PID:g384
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0680w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTKNNNQYNLHNNKSNKTHLTYGTHTSFL---QNCTINDC------VDVDNKDSEIN
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                                           SKTTADDDCVIVAAKDGSDYASSVFDTNSQQKSLASQSTQKELQGHLALTTQESPH---P 703
                                                                                            TNANKENYEKINKNSETTITKSN---
                                                                                                                                                                                                                                 KGKTHSAASTKYGGESTRNGQNIHVLSAEDQCQMETENSVLSHSAKVSPAE---HDIQIM 586
                                                                                                                                                                                                                                                                                                                                                                              EKEKSKDM-----EKLKNKQNDEKKK-----DD-----NEKKKNDKQDIH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSKDKEKEKSKDKEKEKGKDKEKEKSKDI - - - EKEKEKDKDIEKEKSKDTAKEKEKDKDI 403
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                                                                                                                                     SDLHEQSLPKKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQ 646
                                                                                                                                                                                     GNENGSENGNENGNENGNENENKNESENENENENENGNENENEKENEKDKNIKEIENV
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Search completed: September 16, 2002, 22:25:09

Job time: 6498 sec

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              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                   SSNYASRQPVIAPLDRYAERAVNQVHARNFPSTIATMEA/;KLCDRRNAGQVVLYPKESMP
                                                                                                                                   DQYIAEAPTEHW--GRKDAKKLTWEQFKATTRNSPAATC(;AQFRPGIQAVDLTSTHVMGS
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39; Conservative 169;
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-HLLRMMDPSTLASFPNYGTSSRNQME;;QLH--NSQYAHNQYKGSTST
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 128.1 kDa protein in OMP2-MSG5
YNL054W OR N2467 OR YNL2467W.
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97060022; PubMed=8904343;
Bergez P., Doignon F., Crouzet M.;
Yeast 12:297-297(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288C / FY1676;
MEDLINE=96021608; PubMed=8533472;
Bergez P., Doignon F., Crouzet M.;
Bergez P., Doignon et al., Crouzet M.;
The sequence of a 44 420 bp fragment located chromosome XIV from Saccharomyces cerevisiae."
Yeast 11:967-974(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacclaromycetales; Saccharomycetaceae; Saccharomyces
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                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 1165 AA; 128140
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TANTTSNVVQHNLPTIDNNLMDSDATSH-NQDHWHSDINRAGTSMST----SDIPTDLHLE 114
                                                              SGMFSAKWNALQ-LGSVS----
                               NYDVAANVSE-----DNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNED 266
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Pred. No. 0.00055;
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                                                                                                                                          --NFLYLAFVISSLLMTGFILGFLLATNKELQDVD----
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                                                                                                                                                                                            EMBL; AF026032; AAC08741.1; -. EMBL; X99643; CAA67962.1; -. MGD; MGI:103067; Xnp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosomes.";

Proc. Natl. Acad. Sci. U.S.A. 96:13983-13988(1999).

-I- FUNCTION: COULD BE A GLOBAL TRANSCRIPTIONAL REGULGENE EXPRESSION BY AFFECTING CHROMATIN.

-I- SUBUNIT: PROBABLY BINDS EZH2. BINDS ANNEXIN V IN PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSERINE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20040663; pubMed-10570185;
McDowell T.L., Gibbons R.J., Sutherland H., O'Rourke D.N.
Bickmore W.A., Pombo A., Turley H., Gatter K., Picketts
Buckle V.J., Chapman L., Rhodes D., Higgs D.R.;
"Localization of a putative transcriptional regulator (A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               le Douarin B., Nielsen A.L., Garnier J.-M., Ichi
Jeanmougin F., Losson R., Chambon P.,
"A possible involvement of TIF1 alpha and TIF1 b
control of transcription by nuclear receptors.";
EMBO J. 15:6701-6715(1996).
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15-JUL-1999 (Rel. 38, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Transcriptional regulator ATRX (X-linked nuclear (Heterochromatin protein 2) (HPl alpha-interactin
                          Zinc-finger.
ZN_FING
                                                                   SMART; SM00487; DEXDC;
SMART; SM00490; HELICC;
SMART; SM00184; RING; 1
                                                                                                                Pfam;
Pfam;
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"Comparison of the human and murine ATRX conserved, functionally important domains
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Mammalia; Eutheria;
                                                      DNA repair; Nuclear
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InterPro; IPR001410;
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                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SUBCELLULAR LOCATION:
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                                                                                                           PF00271; helicase
PF00176; SNF2_N; 1
                                                                                                                                      IPR001650; Helicas
IPR000330; SNF2_N.
IPR001841; Znf_rin
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1704
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1707
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Rodentia;
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ise_C; 1.
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             ATP
                                                     DNA-binding; Helicase;
                            PHD-TYPE
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Sciurognathi; Muridae;
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Murinae; Mus
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PHQ----VDGVQFMWDCCCESVEKTKKSPGSGCILAHCMGLGKTLQVVSFLHTVLLCDKL
                          PTEHWGRKDAKKLTWE----QFKATTRNSPAATCGAQFRPG----IQAVDLTSTHVMGSSS
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                                                                                                                      DCVIVAAKDGSDYASSVFDTNSQQKS------LASQSTQKELQGHLALTTQESPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQSKTDTAGGEKKGKKWKDKSCEKKEELSDSVDKLPGKGI/SCDSSEDKKTRNRVSLREKK 1072
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19.3%;
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    domain of Hum. Mol.
                                                                                                                                                                                                                                                                       Gibbons R.J., Picketts D.J., Villard L., Higgs D.R.; "Mutations in a putative global transcriptional regulator cause linked mental retardation with alpha-thalassemia (ATR-X syndrometric property).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATRX_HUMAN STANDARD; PRT; 2492 AA. P46100; P51068; Q15886; Q9NTS3; Q9H0Z1; 01-NOV-1995 (Rel. 32, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Transcriptional regulator ATRX (X-linked helicase nuclear protein) (XNP) (Znf-HX).
ATRX OR RAD54L OR XH2.
                                                                                                                                                                      Pearce A., Chapman J
Submitted (DEC-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gecz J., Pollard H., Consalez G., Villard L., Millasseau P., Khrestchatisky M., Fontes M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Determination of the genomic structure a potential zinc finger helicase."; Genomics 43:149-155(1997).
                                           "Specific interaction between the
                                                                   Colleaux L.;
                                                                                     Cardoso C., Timsit
                                                                                                                                                                                                              SEQUENCE OF 1375-2492 FROM N.A.
                                                                                                                                                                                                                                                            Cell 80:837-845(1995).
                                                                                                                                                                                                                                                                                                                                          MEDLINE=95211835; PubMed=7697714
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2401-2492 FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and characterization of a putative helicase.";
                                                                                                         MEDLINE=98167853;
                                                                                                                                 EZH2 BINDING
                                                                                                                                                                                                                                                                                                                                                                                                            Hum. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bianchi M.E.,
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Giovanazzi S., Bossolasco
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MEDLINE=95179111; PubMed=7874112;
Stayton C.L., Dabovic B., Gulisano M.,
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Villard L., Lossi A.-M., Cardoso C.,
Colleaux L., Schwartz C., Fontes M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "ATRX encodes a novel member of the SNF2 family of proteins: point to a common mechanism underlying the ATR-X syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibbons R.J.;
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Mammalia; Eutheria; Primates;
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  of the human E2H2 protein.";
lol. Genet. 7:679-684(1998).
                                                                                                                                                                                                                                                                                                                                                                                                      and expression of the murine homologue nuclear protein gene closely linked to . Genet. 3:39-44(1994).
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                                                                                     PubMed=9499421;
t S., Villard L.
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MEDLINE-99347960; PubMed-10417298;
LOSSÍ A.-M., Millan J.M., Villard L., Orellana C., Cardoso C.,
Prieto F., Fontes M., Martinez F.;
"Mutation of the XNP/ATR X gene in a family with severe mental
retardation, spastic paraplegia and skewed pattern of X inactivation:
demonstration that the mutation is involved in the inactivation
                                                                                                                                                                                                                                                                                                         genotype/phenotype relationship in ATR/X Hum. Mutat. 12:214-214(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibbons R.J., Bachoo S., Picketts D.J., Aftimos S., Asenbauer B., Bergoffen J., Berry S.A., Dahl N., Fryer A., Keppler K., Kurosawa Levin M.L., Masuno M., Neri G., Pierpont M.E., Slaney S.F.,
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chromosomes.";
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Villard L., Bonino M.-C., Abidi F., Ragusa A., Belougne Lossi A.-M., Seaver L., Bonnefont J.-P., Romano C., Ficl Lacombe D., Hanauer A., Philip N., Schwartz C.E., Fontes
                                                                                                                                   VARIANT CWS THR-2050
MEDLINE-99326061; Pul
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Greco D., C
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Munnich A., Lyonnet S.;
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Villard L., Gecz
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"Identification of a mutation in the XNP/
reported as Smith-Fineman Myers syndrome.
Am. J. Med. Genet. 91:83-85(2000).
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                                                                                                                        Abidi
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                                                                                                                                                                                                                                                                                                                                                                                                                              "Mutations in transcriptional regulator of a PHD-like domain.";
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                                                    VARIANTS ATR-X E-175; 178-V--K-198 DEL;
                                                                                              "Carpenter-Waziri syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    point mutation in the XNP gene,
                                                                                                                                                                                                                                                                                                                     era M., Romano C., Castiglia L., Failla P., Ruberto (
o D., Cardoso C., Fontes M., Ragusa A.;
mutations in XNP/ATR-X gene: a further contribution
type/phenotype relationship in ATR/X syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Hum. Genet. 4:316-320(1996).
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Genet. 17:146-148(1997).
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D.R.;
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                                                                                Genet.
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J., Mattei J.-F.,
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85:249-251(1999).
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114 404

Matches

Similarity

Conservative

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-KTSDNGTAPRTLPAKQNGTSDGCSITFVR 144

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Query Match
Best Local
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                                                                                                                                                    use by non-profit institutions a modified and this statement is not removed. Usage by and institutions modified and this statement is not removed. Usage by and institutions and institutions and institutions and institutions are modified by and institutions and institutions are modified by and institutions are modified by and institutions are modified by and institutions are modified by and institutions are modified by and institutions are modified by and institutions are modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modified by an area of the modi
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J. Med. Genet.
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SUBUNIT: PROBABLY BINDS EZHZ. BINDS ANNEXIN V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: UBIQUITOUS.
DISEASE: DEFECTS IN ATRX ARE THE CAUSE OF X-LINKED ALPHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTING WITH HP1.
ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1,
                                                                                                                                                                                                                                         European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                    STATURE AND CRYPTORCHIDISM.
SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY
SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: DEFECTS IN ATRX ARE THE CAUSE OF SUTHERLAND-HAAN MENTAL RETARDATION SYNDROME (SHS). IT IS CHARACTERIZED BY MENTAL RETARDATION WITH SPASTIC PARAPLEGIA, MICROCEPHALY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSERINE-DEPENDENT MANNER (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE AFFECTED BY A VARIANT OF ATR-X SYNDROME
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                                                                U72937; AAB49970.2; -. U72938; AAB49971.2; -. U72935; AAB40698.1; -. U72904; AAB40698.1; JO
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IX MEDLINE=92234949; PubMed=1373717;

Poulsen K., Reinholdt J., Kilian M.;

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Poulsen K., Reinholdt J., Kilian M.;

In fluenzae type 1 immunoglobulin Al proteases.";

L. J. Bacteriol. 174:2913-2921(1992).

L. J. Bacteriol. 174:2913-2921(1992).

L. J. Bacteriol. 174:2913-2921(1992).

L. J. Bacteriol. 174:2913-2921(1992).

L. J. Bacteriol. 174:2913-2921(1992).

L. PUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNOGLOBULIN A PRODUCING INTACT FC AND FAB FRAGMENTS.

L. POUNCTION: VIRULENCE FACTOR; CLEAVES HOST IMMUNOGLOBULIN A PRODUCING INTACT FC AND FAB FRAGMENTS.

L. POUNCTION: CLEAVES HOST IMMUNOGLOBULIN A PRODUCING AND THE SECRETION OF THE PERIPLASMIC SPACE, AND THE CARROXY-TERMINAL HELPER DOMAIN ASSOCIATES WITH THE COUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE
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01-NOV-1995
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SIMILARITY: BELONGS TO PEPTII
  SRRTRRSVQTN----
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                                             NFQSTQEQQTHLRMEEMVTIAASSPLFSHHDDQYIAEAPTEHWGRKDAKKLTWEQFKATT
                                                                                                                                                 DDCVIVAAKDGSDYASSVFDTNSQQKSLASQSTQKELQGHLALTTQE-----SPHPQ
                                                                                                                                                                                                                                                 SLPKKKKKQKLEVTREKQTMIDDIPMDIVELLAKNQHERQLMTETDCSDINRIQSKTTAD
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-ELPTEN-
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                                                                                            Uemori T., Shimojo T., Asada K., Asano
Maki M., Hatanaka M., Murachi T., Hanza
"Characterization of a functional doma"
                                                                                                                         MEDLINE-90165962;
                                                                                                                                                                                           SEQUENCE OF 101-317 FROM N.A. MEDLINE=90037002; PubMed=2553724;
                                                                                                                                                                                                                                  "Molecular diversity in by exon skipping.";
                                                                                                                                                                                                                                                                                                                                  Kato
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Mammalia; Eutheria;
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Lee W.J., Ma H.,
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           MEDLINE-95038502; PubMed-7951045;
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Enzym. Inhib. 3:49-56(1989).
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   Wei S.G.,
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Adachi Y.,
Hatanaka M.
                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91139699;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          hematopoietic system cells.";
J. Biol. Chem. 266:3968-3972(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Phosphorylation and subcellular distribution of calpastatin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Calpastatin gene in human testis.
Biochem. Mol. Biol. Int. 33:245-25
                                                                                                                                                                                                                                                  BIOL. Chem. 266:3968-3972(1991).

FUNCTION: SPECIFIC INHIBITION OF CALDAIN (CALCIUM-DEPENDENT FUNCTION: SPECIFIC INHIBITION OF CALDAIN (CALCIUM-DEPENDENT FUNCTION).

CYSTEINE PROTEASE). PLAYS A KEY ROLE IN POSTMORTEM TENDERIZATION OF MEAT AND HAVE BEEN HYPOTHESIZED TO BE INVOLVED IN MUSCLE PROTEIN DEGRADATION IN LIVING TISSUE.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

DOMAIN: HAS FOUR INHIBITORY DOMAINS.

PTM: THE N-TERMINUS IS BLOCKED.
                                                                                                                                                                                                                                          PTM: PHOSPHORYLATED.
D16217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishida-Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425-708
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                                                                     (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c.,
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InterPro; IPR001259; Calpain_inhib.
Pfam; PF00748; Calpain_inhib; 4. Repeat; Thiol p Phosphorylation A34428; A34428 114090; -. M28230; M28227; M28228; M28229; M38229; M33229; U26724; S73329; U38525; U31345; U31346; D50827; M86258; 467 486 543 170 304 446 583 212 592 AAA52066.1; AAA52066.1; AAA52066.1; AAA52066.1; AAA52066.1; AAA52066.1; AAA52066.1; AAA52136.2; AAB32311.1; AAAB0684.1; AAB60371.1; AAB60372.1; BAA03747.1; BAA09438.1; AAB59398.1; protease 169 222 356 499 636 224 592 467 488 543 inhibitor; JOINED.
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ID MAPB_H
AC P46821
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DT 16-OCT
DE Microt
DE LC1].
GN MAPB_B.
OS Homo s
OC Eukary
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01-NOV-1995
01-NOV-1995
16-OCT-2001
Eukaryota;
                                                                                     Microtubule
                                                                                                                                                                                MAPB_HUMAN
                           Homo sapiens (Human
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SEQUENCE
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                                                                                                                                                                                                                                                                                                     VFDTNSQQ-----KSLASQSTQKELQGHL---ALTTQESPHPQN 705
                                                                                                                                                                                                                                                                                                                                                                           TMIDD-IPMDIVELLAKNQHERQLMTETDCSDINRIQSK: TADDDCVIVAAKDGSDYASS
                                                                                                                                                                                                                                                                                                                                        GERDDTIPPEYRHLLDDNGQDKPVKPPTKKSE----DSKKPADDQDPIDALSGDLDSCPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDTENGLDTNMHKTDVCQHVSEISTQRCSSKGKTAGLSK;KTHSAASTKYGGESTRNGQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGPQNASSLKFEDAKLAAAISEVVSQ------TPASTTQAGAPPRD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVSDPMSSTYIEELGKREVTIPPKYRELLAKKEGITGPPADSSKPIGPDDAIDALSSDFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EV--PQITWHIEVNGADQPPSTPKLSEVVLKR--------------
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         Metazoa;
                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation updat
-associated protein 1B (MAP 1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562
708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RTGSVHHTV-----AHPAGNLSNKKVTPTASTQH------DDE
                                                                                                                                                                            STANDARD;
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       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 J
76484 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 197; No. 0.
     Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISSING (IN REN. 8).
; CACD759C9284N3EA CRC64;
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                            2468
                                                                                                   update)
                                                                           1B) [Contains:
   Vertebrata;
                                                                                                                                                                           B
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.00:1;
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                                                                                                                                                                                                                                                                    707
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   Euteleostomi;
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                                                                           MAP1 light chain
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REPEAT
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REPEAT
                   612
                                                                                             564
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MIM; 157129; -.
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TISSUE=Fetal brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                              KNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANTDS--PMKDLQGPAQNYDVAANVSEDN
                                                                                                                      TSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLKRNEDENGKTEETLVAEQCNLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO MAPIA.
                                                DPNPMSGKERDQVAEQCNLTKDPKPVSG-----QKCEQICNEPCEEVVLKRSSKSKRKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of MAPIB (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STABILIZING MICROTUBULES.
                                                                                                                                                             KHLDFLKQPLATQKDLTGQVPTPVVKQTKLKQRADSRESLKPAAKPLPSKSVRKESKE--
                                                                                                                                                                                                                                             204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00414; MAP1B
                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000102; MAP1B_neuraxin.
                                                                                                                                                                                                                                                                                                                                                                         1878
1895
1912
1929
1946
1963
1997
2014
2031
2048
                                                                                                                                                                                                                                                                                                                                    2468
                                                                                                                                                                                                                                           Conservative
             -KAEVAEK--QATDVKPKAAKEKTVKKETKVKPEDKKEEKEKPKKEVAKKED
                                                                                     ETPEVT - - - KVNHVEKPPKVESKEKVMVKKDKPVKTETKPSVTEKEVPSKE
                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAP1B_NEURAXIN; 6.
                                                                                                                                                                                                                                                                                                                                                                         1894
1911
1928
1945
1962
1979
2013
2003
2047
2064
790
                                                                                                                                                                                                                                                        3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                    270618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuraxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation
                                                                                                                                                                                                                                         170;
                                                                                                                                                                                                                                                                                                                                    MΨ
                                                                                                                                                                                                                                                          Score 196.5; DB Pred. No. 0.016;
                                                                                                                                                                                                                                                                                                                                                  MAP1B 10.
LYS-RICH
KKEE AND
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MAP1B
MAP1B
MAP1B
MAP1B
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MAP1B 2.
MAP1B 3.
MAP1B 4.
MAP1B 5.
MAP1B 6.
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MAP1B 8.
MAP1B 8.
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                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                        DB 1;
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В Q 밁 δÃ 밁 Q 밁 Q В Qγ 밁 Ş В δÃ

Indels Length

Gaps

44;

224

611 284

2468 289;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Fetal brain,
MEDLINE=95104835; PubMed=7806212;
Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
Cloning of human microtubule-associated protein
"Cloning of human microtubule associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: Has a nighty basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules. PTM: LC1 is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteolytic processing. It is free to associate with both MAPIA and MAPIB. It interacts with the amino-terminal region of MAPIA PLAY similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAP1A AND MAP1B PROTEINS.

DOMAIN: Has a highly basic region with many copies of the sequence proper and weather the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the s
-RICH (HIGHLY BASIC, CONTAINS E AND KKEI/V REPEATS). 540839CBDF09D461 CRC64;
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ANK2_HUMAN STANDALL,
Q01484: Q01485;
Q1-APR-1993 (Rel. 25, Created)
Q1-CTT-1996 (Rel. 34, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CTT-2001 (Rel. 40, Last annotation update)
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Interpro; IPR002110; ANK, R Interpro; IPR000408; Death, R Interpro; IPR000906; ZU5. R Pfam; PF00023; ank; 24. Pfam; PF00791; death; 1. Pfam; PF00791; ZU5; 1. PF10791; SMART; SM00005; DEATH; 1. SMART; SM00005; DEATH; 1. SMART; SM000218; ZU5. 1
                                                                                                                                                      PIR; S14533; S14533.
PIR; A39643; A39643.
PIR; B39643; B39643.
PIR; S14569; S14569.
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between
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                                                                                                                                                                                                                                                                     use by non-profit institutions as lone modified and this statement is not remove entities requires a license agreement (so or send an email to license@isb-sib.ch).
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Tse W.T., Menninger J.C., Yang-Feng T.L.
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chan W., Kordeli E., Bennett V.; "440-kD ankyrinB: structure of the madomain and selective localization in
                                                                                                                               MIM; 106410;
                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Otto E., Kunimoto M., McLaughlin T., Bennett V.;
"Isolation and characterization of cDNAs encoding
ankyrins reveal a family of alternatively spliced
J. Cell Biol. 114:241-253(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ankyrins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain stem;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffed and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                      AND FUNCTION (POTENTIAL).
SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Attach integral membrane proteins to elements. Also bind to cytoskeletal proteins. ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS CELLS THROUGHOUT THE BRAIN.

PIM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFER
                                                                                                                                                                                                                                                                                                                                                                                                            AND
                                                                                                                                                                                                         X56957; CAA40278.1;
X56958; CAA40279.2;
Z26634; CAB42644.1;
M37123; AAA62828.1;
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Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chackers of the second control of the second control of the sec
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-i- SIMILARITY: SOME, TO MAMMALIAN NEUROFILAMENT TRIPLET M PROTEIN
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Guillonneau X., Piriev N.I., Danciger M., Ko
Jacobson S.G., Farber D.B.;
"A nonsense mutation in a novel gene is asso
pigmentosa in a family linked to the RPI loc
Hum. Mol. Genet. 8:1541-1546(1999).
-i- FUNCTION: COULD HAVE A ROLE IN THE DIFFE
PHOTORECEPTOR CELLS.
-i- TISSUE SPECIFICITY: EXPRESSED IN RETINA.
BRAIN, PLACENTA, LUNG, LIVER, SKELETAL M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000
30-MAY-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                    MEDINE-99318096; PubMed-10391212; MEDINE-99318096; PubMed-10391212; Sullivan L.S., Heckenlively J.R., Bowne S.J., Zuo Gal A., Denton M., Inglehearn C.F., Blanton S.H., "Mutations in a novel retina-specific gene cause a retinitis pigmentosa."; Nat. Genet. 22:255-259(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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01-MAR-2002 (Rel. 41, Last annotation update)
Oxygen-regulated protein 1 (Retinitis pigmentosa
(Retinitis pigmentosa 1 protein).
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                                                                                                                              SEQUENCE FROM N.A. MEDLINE-99330563; PubMed-10401003;
                                                                                                                                                                                                                                 MEDLINE-99318095; PubMed-10391211;
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AND TYR-2033.
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Query Match
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         264 NEDEN-----GKTEET---LVAEQCNLTKDPNPM---SGKE----
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DISEASE: DEFECTS IN RP1 CAUSE RETINITIS PIGMENTOSA FORM 1 (RP1); IDISEASE: CHARACTERIZED BY CONSTRICTION OF THE VISUAL FIELDS, NIGHT BLINDNESS, AND FUNDUS CHANGES. THE DISEASE SEEMS TO BE ASSOCIATED HAVE A CONTRACTED (STOP OR FRAMESHIFT MUTATIONS) FORMS OF THE
                                                                         -----DIEKSIIFNQDGT
                                                                                                     GPAQNYDVAANV--SEDNTSVDVGALPEVPQITWHIEVNGADQPPSTPKLSEVVLK---R
                                                                                                                                                                            GSQKVSPSTQSSQGKNA--DRSTLPKS--VQEGNDSKCNAPSGKNGAAEANTDSPMKDLQ
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DATABASE: NAME-Mutations of the RP1 gene;
NOTE-Retina International's Scientific Newsletter;
NWW-"http://www.retina-international.com/sci-news/rplmut.htm"
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SIMILARITY: CONTAINS 2
DATABASE: NAME=RetNet;
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                                                                                                                                            MAPB RAT

P15205; Q62958; Q9ER21; Q9QW92;

01-APR-1990 (Rel. 14, Created)

f 16-OCT-2001 (Rel. 40, Last sequence update)

T 16-CCT-2001 (Rel. 40, Last annotation update)

E Microtubule-associated protein 1B (MAP 1B) (NE light chain LC1).
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SEQUENCE OF 1-142 FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Testis;
MEDLINE-98257242; PubMed-8666295;
                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                      1012
                                                                             NCBI_TaxID=10116,
                                                                                                                                    Rattus norvegicus
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                                                                                             Craniata; Ver
Sciurognathi;
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P 1B) (Neuraxin)
                                                                                           Vertebrata;
thi; Muridae;
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593

QKSDTVI

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1046 984

1011

971 882 926 822 880 763 830 703

Euteleostomi; ; Murinae; Rat

Rattus

[Contains:

MAP1

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RX MEDLINE-97405699; PubMed-9260743;
RA Ma D., Nothias F., Boyne L.J., Fischer I.;
RT Ma D., Nothias F., Boyne L.J., Fischer I.;
RT Thifferential regulation of microtubule-associated protein 1B (MAP1B)
RT in rat CNS and PNS during development.*;
RI J. Neurosci. Res. 49:319-332(1997).
C. Pinorion: The function of brain MAPS is essentially unknown.
C. Phosphorylated MAP1B may play a role in the cytoskeletal changes that accompany neurite extension. Possibly MAP1B Binds to at least C. two tubulin subunits in the polymer, and this bridging of subunits might be involved in nucleating microtubule polymerization and in stabilizing microtubules.
C. Insubunit: 3 different light chains, LC1, LC2 and LC3, can associate with MAP1B and MAP1B proteins.
C. ITISSUE SPECIFICITY: Nervous system (spinal cord, brain stem, cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                             or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J., Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H "Neuraxin, a novel putative structural protein of the rat cent nervous system that is immunologically related to microtubule-associated protein 5."; EMBO J. 8:2879-2888(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and sequencing associated protein (MAP1B) Gene 172:307-308(1996).
                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zauner W., Kratz J., Staunton J., Feick P., "Identification of two distinct microtubule recombinant rat MAP 1B.";
                                                                 EMBL; U52950; AAB17068.1;
EMBL; X60370; CAC16162.1;
EMBL; X16623; CAA34620.1;
EMBL; S06017; S06017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Spinal cord; MEDLINE-90059871; PubMed-2555150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 96-2459 FROM N.A.,
             InterPro; IPR000102; MAP1B_neuraxin. Pfam; PF00414; MAP1B_neuraxin; 10. PROSITE; PS00230; MAP1B_NEURAXIN; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92347374; PubMed=1639092;
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                                                                                                                                                               :ities requires a license agreement (See http://www.isb-sib.ch/announce/
send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                      nerve levels are high early in development but decrease during postnatal development and are low in adults. In dorsal root ganglia levels remain high throughout development.

INDUCTION: By nerve growth factor.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PTM: LC1 is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteolytic processing. It is free to associate with both MAPIB and MAPIB. It interacts with the amino-terminal region
                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                             CAUTION: A C-terminal fragment of this protein (residues 1597 2459) was originally described as neuraxin in ref.3.
                                                                                                                                                                                                                                                                                                                                                    PTM: Phosphorylated.
SIMILARITY: TO MAPIA.
                                                                                                                                                                                                                                                                                                                                                                                      of MAP1B (By similarity).
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                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heart or muscle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. 57:66-74(1992).
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SEPTPMDEMSTPRDVMTDETNNEETESPSQEFVNITKYESSLYS---QEYSKPVVASFNG
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                   -- PHPQNFQS
                                        PAKQPGVQSPSREPASSIHDETLPGGSESEATASDEENREDQPEEFTATSGYTQSTIEIS
                                                                                EKGEAEQSEEEGEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDKAAEAGVTEDQYDFLGT
                                                                                                     AK - - - NQHERQLMTETDCSDINRIQ - - - - SKTTADDDCVIVAAK - - -
                                                                                                                                               ENSVLSHSAKVSPAEHDIQIMSDLHEQSLPKKKKKQKLEVTREKQTMIDD-IPMDIVELL
                                                                                                                                                                     TEGEGECEQTPEELEPVEKQGVDDIEKFEDEGAGFEESSEAGDYEEKAETEEAEEPEEDG
                                                                                                                                                                                         TKYGGESTRNGQNIHVLSAE
                                                                                                                                                                                                              DFEELKAEEIDVAKDIKPQLELIEDEEKLKETEPGEAYVIQKETEVSKGSAESPDEGITT
                                                                                                                                                                                                                                                                             KYSDVVDDGSSLMNWLNGKKKRTGSVHHTVAHPAGNLSN---KKVTPTASTQHDDENDTE
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                                                                                                                                                                                                                                                                                                                                            EDKTPLKKDEKPKKEEAKKEI - - - KKEIKKEEKKELKKEVKKETPLKDAKK - EVKKDEKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TSVDVGALPEVPQITWHIEVNGADQPPSTPKL---SEVVLKRNEDENGKTEE--TLVAEQ
                                                                                                                           EDNVSGSASKHSPTE-
                                                                                                                                                                                                                                    NGLDTNMHKTDVCQHV-----AAS
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                  -----TQEQQTHLRMEEMVTIAA-SSPLFSHHDDQYIAEAPTEHWG
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1936
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2004
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                                                           -ASSVEDT ---- NSQQKSLASQSTQKELQ
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LYS-RICH.
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T -> S (I
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MAP1B 2.
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MAP1B 4.
MAP1B 6.
MAP1B 7.
MAP1B 9.
MAP1B 9.
MAP1B 9.
GLU-RICH.
LYS-RICH
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S (IN REF.
K (IN REF.
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RESULT 12
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                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
 EMBL; L06487;
                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                   STRAIN-BR1824-3B;
MEDLINE-93161412; PubMed-7916652;
Sym M., Engebrecht J.A., Roeder G.S.;
"ZIP1 is a Synaptonemal complex protein chromosome synapsis.";
Cell 72:365-378(1993).
[2]
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01-0CT-1996 (Rel. 34, Last sequenc
15-JUL-1998 (Rel. 36, Last annotat
Synaptonemal complex protein ZIP1
ZIP1 OR YDR285W OR D9819.9.
                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP1_YEAST
P31111;
                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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AAA35239.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                       (See http://www.isb-sib.ch/announce,
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Query Match
Best Local Similarity
Matches 161; Conserv
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PIR; A45173; A45173.
PIR; S30868; S30868
SGD; S0002693; ZIP1.
Nuclear protein; Meiosis; C
DOMAIN 177 333
DOMAIN 397 438
DOMAIN 456 752
CONFLICT 55 55
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RMMDPSTLASFPNYGTSSRNQMESQLHNSQYAHNQYKGSTSTSYGSNLNGKIPL 912
                                     SQKRELEQKIKELEEIKNHKRNEPSKKGTQNFTKPSDSPKKNATTSNLFPNNS-AAIH--
                                                                         PLDRYAERAVNQV-----HARNFPSTIATMEASKLCD--RRNAGQVVLYPKESMPATHLL
                                                                                                                E-SLSDVKTLKQQVIVLKSEKQDITAEKLELQDNLESLEEVTKNL------QQKVQ
                                                                                                                                                                                         KENEQKDHTTKLEAFQKNNEQLQKLNVE--VVQLKAHELELEEQNRHLKNCLEKKETGVE
                                                                                                                                                                                                                                                                LSNELKKVQDQLEKLNNLNITTK---SNYENKISSQNEIVKALVSENDTLKQRIQQLVEI 618
                                                                                                                                                  HWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIA 805
                                                                                                                                                                                                                             TTQE----SPHPQNFQSTQEQQTHLRMEEMVTIAASSPLFSHHDDQYI-----AEAPTE 745
                                                                                                                                                                                                                                                                                                    -CSDINRIQSKTTADDDCVIVAAKDGSDYASSVFDTNSQQKSLASQ--STQKELQGHLAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -RQNHQLYQRRISGFKTSIENLNKTINDL-----GKNKKEADAELMKKGKEIEYLKRELD
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333 COILED COIL (POTENTIAL).
438 COILED COIL (POTENTIAL).
752 COILED COIL (POTENTIAL).
55 T -> A (IN REF. 1).
100035 MW; 674F12625CD9DDFD CRC64;
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SPMKKCPKVDHISKSRINSSKETSKF-NDEFDLSSSSNDDLELTNPSPI

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HESULA DE RESULA   Query Match
Best Local Similarity
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MAPB_MOUSE STANDARD

P14873;
01-APR-1990 (Rel. 14, L.

01-APR-1990 (Rel. 14, L.

01-MAR-2002 (Rel. 41, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B)
[Contains: MAP1 light chain LC1].
MAP1B OR MTAP1B OR MTAP5.
Mus musculus (Morror)
                                                                                                                                                                          REPEAT
REPEAT
                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The microtubule binding domain of microtubule-associated properties a repeated sequence motif unrelated to that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND DOMAIN.
STRAIN-SWISS WEBSTER; TISSUE-Brain;
MEDLINE-90094539; Pubmed-2480963;
Noble M., Lewis S.A., Cowan N.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                      REPEAT
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                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Biol. 109:3367-3376(1989).

- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.

- PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST
TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS
MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAPIA AND MAPIB PROTEINS.

DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PTM: LC1 IS COEXPRESSED WITH MAPIB. IT IS A POLYPEPTIDE GENERATED FROM MAPIB BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIA AND MAPIB. IT INTERACTS WITH THE AMINO-TERMINAL REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tau.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; x51396; CAA35761.1;
S07549; QRMSP1.
MGI:1306778; Mtap1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro; IPR000102; MAP1B_neuraxin. PF00414; MAP1B_neuraxin; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       PS00230; MAP1B
                                                                                       2464
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1891
1908
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Score
Pred.
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MAP1B 1.
MAP1B 2.
MAP1B 3.
MAP1B 4.
MAP1B 5.
MAP1B 7.
MAP1B 8.
MAP1B 8.
                                                                                                          MAP1B 10
LYS-RICH
KKEE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; | Sciurognathi; Muridae;
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                                                                                     RICH (HIGHLY BAS
AND KKEI/V REPE
FBD3DD99CFDBDA87
                                                                                                                                                                                                                                                                                                                                                                            LIGHT
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182.5; DB No. 0.086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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Length

RESULT 14
P531_HUMAN
ID P531_H
AC Q12888
DT 15-JUL
DT 16-OCT

P531_HUMAN Q12888;

STANDARD;

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15-JUL-1998 16-OCT-2001

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VVSPSQSVTGSAGHTPYYQSPTDEK
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                                                                                           GSLLQKEIANWS----ENCGTQSGYKLGVSTGITSHQMNRKEHFEALNSGMFSAKWNALQ
                                                                                                                           SPPSSMEEDKFSKSALRDAYCSEEKELKASAELDIKDVSDERLSPAKSPSLSPSPPSPIE 126:
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                                                              KTPLGERSVNFSLTPNEIKVSAEGEARSVSPGVT - - QAVVEEH
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Best Local S
Matches 180
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Pfam; PF00533; BRCT; 4.

SMART; SM00392; BRCT; 2.

PROSITE; PS50172; BRCT; 2.

PROSITE; PS50172; BRCT; 2.

PROSITE; PS50172; BRCT; 2.

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PROSITE: PS50172; BRCT; 2.

PROSITE: PS70172; BRCT; 2.

PROSITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98421532; PubMed-9748285; Iwabuchi K., Li B., Massa H.F., Trask B.J., I "Stimulation of p53-mediated transcriptional p53-binding proteins, 53BP1 and 53BP2."; J., Biol. Chem. 273:26061-26068(1998).
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TISSUE=Skeletal musi
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Mammalia; Eutheria;
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nilarity 18.6%;
Conservative 13!
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Metazoa; Chordata; C
Metazoa; Primates; (
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B BRCT 1.

54 BRCT 2.

16 POLY-SER.

54 POLY-GLU.

213573 MW; 13E2CC8A265F9D2A CRC64;
                                                             ----IPVTAQPSKDVHVVKEQNPPPARSEDMPFSPKASVAA
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Catarrhini; Hominidae
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                                   "CENP-E mitosis.
                                       SEQUENCE FROM N.A.

MEDLINE-93024922; PubMed-1406971;

Yen T.J., Li G., Schaar B.T., Szii

"CENP-E is a putative kinetochore
mitosis.";
CHARACTERIZATION
                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                               01-JUL-1993
30-MAY-2000
                         Nature
                                                                                                                                                                   Centromeric
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01-JUL-1993
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                     359:536-539(1992).
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                                                                                                                                                                                                                                                                                          873
                                                                                                                     Primates;
                                                                                                                             Chordata;
                                                                                                                                                                 Last sequence upon Last annotation (CENP-E protein)
                                                                                                                                                                                                      Created)
                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                         Szilak
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                                              motor
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Best Local Sin
Matches 185;
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Chan G.K.T., Schaar B.T., Yen T.J.;

Chan G.K.T., Schaar B.T., Yen T.J.;

Chan G.K.T., Schaar B.T., Yen T.J.;

Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBR1.";

J. Cell Biol. 143;49-63(1998).

J. Cell Biol. 143;49-63(1998).

-I- FUNCTION: MINIS-END DIRECTED MICROTUBULE MOTOR. PROBABLE KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOS. ST THE G2 PHASE OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT AND/OR SPINDLE ELONGATION.

-I- SUBCRLIULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
                                                                           1974
                                                                                                                                                     1926
                                                                                                                                                                                                                            1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle; Centromere.
DOMAIN 1 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z15005; CAA78727.1; -. PIR; S28261; S28261. HSSP; P17119; 3KAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95196755; pubMed=7889940; Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.; "Mitotic HeLa cells contain a CENP-E-associated minus end-directed microtubule motor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE-98437347; PubMed-9763420;
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     2025
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                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                               31 VLELTATPRQDAAAEAGVDEPAQHQCEHFSIRGYV----ALLQKKDPKFCSLSRIFHDQK 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                              DSPMKDLQGPAQNYDVAANVSEDNTSVDVGALPEVPQITWHIEVN-----GADQPPSTPK : |: |: | | | | | | |
                                                                                                                                                                                                                     NLEEMK-----SVMKERDNLRRVEETLKLERDQLKESLQETKARDLEIQQE-----
                                                                                                                                                                                                                                            KCDEHKASSSPFSVAK----FRRWDCSKCL--DKLKTSDNGTAPRTLPAKQNGTSDGCSI 140
LHESLEEIRIVAKERDELRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQ
                                  LSEV-----VLKRNEDENGKTEETLVAEQCNLTKDPNPMSGKERD--QVAEQCNLTKDPK 308
                                                                           ELQKKELQ.
                                                                                                                                                                                TFVRSTFVPASVGSQKVSPSTQSSQGKNADRSTLPKSVQEGNDSKCNAPSGKNGAAEANT 200
                                                                                                                                                                                                                                                                                              IQELKANEHQLITLKKDVNETQKKVSEMEQLKKQIKDQSLTLSKLEIENLNLAQELHE-- 1879
                                                                                                                                               -----LKTARMLSKEHKETVDKLREKISEKTIQISDIQKDLD-----KSKDELQKKIQ 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14:918-926(1995).
                                                                                                                                                                                                                                                                                                                                                                      Similarity 18.9
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>Α</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 ATE
312087 MW;
                                                                                                                                                                                                                                                                                                                                                                                        3.3%;
                                                                     -LLRVKED-VNMSHKKINEMEQLKKQFEPNYLCKCEMDNFQLTKK
                                                                                                                                                                                                                                                                                                                                                                        155;
                                                                                                                                                                                                                                                                                                                                                                                        Score 181.5; D
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KINESIN-MOTOR.
COILED COIL (POTENTIAL).
GLOBULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEFC13880C8C8CB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                      357;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                      283;
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                            255
                                                                       2024
                                                                                                                                                                                                                       1925
                                                                                                                                                                                                                                                                                                                                                                      45;
```

	SSLGLCPEVQNAGAESVDSQ 2645	2626	DЬ
	STLASFPNYGTSSRNQMESQ 883	864	Qy
2625	P	2585	DЬ
863	PLDRYAERAVNQVHARNFPSTIATMEASKLCDRRNAGQVVLYPKESMPATHLLRMMDP	806	Qy
2584	TWKERTLKREAHKQVTCENSPKSPKVTGTASKKKQIT	2548	Db
805	HWGRKDAKKLTWEQFKATTRNSPAATCGAQFRPGIQAVDLTSTHVMGSSSNYASRQPVIA 805	746	Qy
2547	TCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQNEQLIKQKNELLSNNQHLSN-EVK 2547	2491	Db
745	TAASSPLFSHHDDQYIAEAPTE 745	706	Qy
2490		2444	망
705	ADDDCVIVAAKDGSDYASSVFDTNSQQKSLASQSTQKELQGHLALTTQESPHPQN 705	651	Qy
2443	KETIQVLQDKVALGAKPYKEEIEDLKMKLVKIDLEKMKNAKEFEKE	2398	Db
650	KQKLEVTREKQTMIDDIPMDIVEL-LAKNQHERQLMTETDCSDINRIQSKTT	600	Qy
2397	TQLTTEKIRELENSLHEAKESAMHKESKIIKMQKELEVTNDIIAKLQAKVHESNKCLEKT	2338	DЪ
599		559	Qy
2337	KEWEQDLKSLKEKNEKLFKNYQTLKT-SLASGAQVNPTTQDNKNPHVTSRA 2337	2288	ф
558	Œ	503	Qy
2287	NTRFDIEKLKNGIQKENDRICQVNNFFNNRIIAIMNESTEFEERSATIS	2239	рь
502		455	Qy
2238	DLKLNQNMDLHIEEILKDFSESEFPSIKTEFQQVLSNRKEMTQFLEEWL	2190	Db
454	PCEDDRSTIPVPMEVSMDIPVSNHTVGEDGLKSSKNKTKRKYSDVVDDGSSLMNWL	399	Qy
2189	YVTKIKEEQHECINKFEMDFIDEVEKQKELLIKIQHLQQDCDVPSRELR	2141	Db
398	MKKQQHSKKRTAQADVSDAKLCRRKPKKVRLLSEIINANQVEDSRSDEVHRENAAD	343	Qy
2140	QHLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFHRIMKKLKYVLS 2140	2085	Db
342		309	Qy

Search completed: September 16, 2002, 22:35:04 Job time: 658 sec

Coloson Mario Hand SIAL SIAL